

H1CDR (26) GFNIKDSYMH (35)
H2CDR (50) WIDPENGDT EYAPKFQ (65)
H3CDR (99) GTPTGPYYFDY (109)
L1CDR (159) SASSSVSYMH (168)
L2CDR (184) STSNLAS (190)
L3CDR (223) QQRSSYPLT (231)

Fig. 1. Amino acid sequences of CAB1 CDRs

SEQ ID NO: 1

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1  QVKLQQSGAE LVRSGTSVKL SCTASGFNIK DSYMHWLRQG PEQGLEWIGW
51  IDPENGDT EY APKFQ GKATF TTDTS SNTAY LQLSSLTSED TAVYYCNEGT
101 PTGPYYFDYW GQGTTVT VSS GGGGSGGGGS GGGGSENVLT QSPAIMSASP
151 GEKVTITCSA SSSVSYMHWF QQKPGTSPKL WIYSTSNLAS GVPARFSGSG
201 SGTSYSLTIS RMEAEDAATY YCQQRSSYPL TFGAGTKLEL KRAATPVSEK
251 QLAEVVANTI TPLMKAQSVR GMAVAVIYQG KPHYYTFGKA DIAANKPVTP
301 QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351 LDLATYTAGG LPLOVPDEVT DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401 LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451 KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501 SRYWRIGSMY QGLGW EMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551 PVKASWVHKT GSTGGFGSYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601 LEALQ
```

Fig. 2A Amino acid sequence of CAB1 protein

SEQ ID NO: 2

1 TPVSEKQLAE VVANTITPLM KAQSVPGMAV AVIYQGKPHY YTFGKADIAA
51 NKPVTPQTLF ELGSISKFTT GVLGGDAIAR GEISLDDAVT RYWPQLTGKQ
101 WQGIRMLDLA TYTAGGLPLQ VPDEVTDNAS LLRFYQNWQP QWKPGTTRLY
151 ANASIGLFGA LAVKPSGMPY EQAMTTRVLK PLKLDHTWIN VPKAEEAHYA
201 WGYRDGKAVR VSPGMLDAQA YGVKTNVQDM ANWVMANMAP ENVADASLKQ
251 GIALAQSRYW RIGSMYQGLG WEMLNWPVEA NTVVETSFGN VALAPLPVAE
301 VNPPAPPVKA SWVHKTGSTG GFGSYVAFIP EKQIGIVMLA NTSYPNPARV
351 EAAYHILEAL Q

Fig. 2B Amino acid sequence of BLA protein

SEQ ID NO: 3

H1CDR (26) GFNIKDSYMH (35)
H2CDR (50) WIDPENGDT EYAPKFQ (65)
H3CDR (99) GLPTGPYYFDY (109)
L1CDR (159) SASSSVSYMH (168)
L2CDR (184) DTSNLAS (190)
L3CDR (223) QQRDSYPLT (231)

Fig. 3A Amino acid sequences of CAB1.6 CDRs

H1CDR (26) GFNIKDSYMH (35)
H2CDR (50) WIDPENGDT EYAPKFQ (65)
H3CDR (99) GLPLGAIYNDY (109)
L1CDR (159) SASSAVYAMH (168)
L2CDR (184) DTSNLAS (190)
L3CDR (223) QQRDSYPLT (231)

Fig. 3B Amino acid sequences of CAB1.7 CDRs

1	QVQLQQSGAE	LVKSGGSVKL	SCTASGFNIK	DSYMHVVRQG	PEQGLEWIGW
51	IDPENGDEY	APKFQ GKATF	TTDTSSNTAY	LQLSSLTSED	TAVYYCNEGL
101	PTGPYYFDYW	GQGTTVTVSS	GGGGSGGGGS	GGGGSENVLT	QSPAIVSASP
151	GEKVTITCSA	SSSVSYMHWF	QQKPGTSPKL	VIYDTSNLAS	GVPARFSGSG
201	SGTSYSLTIS	RMEAEDAATY	YCQORDSYPL	TFGAGTKLEL	KRAATPVSEK
251	QLAEVVANTI	TPLMKAQSVP	GMAVAVIYQG	KPHYTYFGKA	DIAANKPVTP
301	QTLFELGSIS	KTFTGVLGSD	AIARGEISLD	DAVTRYWPQL	TGKQWQGIRM
351	LDLATYTAGG	LPLQVPDEVT	DNASLLRFYQ	NWQPQWKPGT	TRLYANASIG
401	LFGALAVKPS	GMPYEQAMTT	RVLKPLKLDH	TWINVPKAE	AHYAWGYRDG
451	KAVRVSPGML	DAQAYGVKTN	VQDMANWVMA	NMAPENVADA	SLKQGIALAQ
501	SRYWRIGSMY	QGLGWEMLNW	PVEANTVVET	SFGNVALAPL	PVAEVNPPAP
551	PVKASVVKHT	GSTGGFGSYV	AFIPEKQIGI	VMLANTSYPN	PARVEAAYHI
601	LEALQ				

Fig. 4A Amino acid sequence of CAB1.6 protein

SEQ ID NO. 7

1 QVQLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWVRQG PEQGLEWIGW
51 IDPENGDTHEY APKFQGKATF TTDTSNTAY LQLSSLTSED TAVYYCNEGL
101 PTGPYYFDYW GQGTTVTVSS GGGGSGGGGS GGGGSENVLT QSPAIVSASP
151 GEKVTITCSA SSSVSYMHWF QQKPGTSPKL VIYDTSNLAS GVPARFSGSG
201 SGTSYSLTIS RMEAEDAATY YCQQRDSYPL TFGAGTKLEL KRAATPVSEK
251 QLAEVVANTI TPLMAAQSVPM GMAVAVIYQG KPHYITFGKA DIAANKPVTP
301 QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351 LDLATYTAGG LPLQVPDEVTD DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401 LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451 KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501 SRYWRIGSMY QGLGWEMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551 PVKASWVHKT GSTGGFGAYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601 LEALQ

Fig. 4B Amino acid sequence of CAB1.6i protein

SEQ ID NO: 8

1 QVQLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWVRQG PEQGLEWIGW
51 IDPENGDTHEY APKFQGKATF TTDTSNTAY LQLSSLTSED TAVYYCNEGL
101 PLGAIYNDYW GQGTTVTVSS GGGGSGGGGS GGGGSENVLT QSPAIVSASP
151 GEKVTITCSA SSAVYAMHWF QOKPGTSPKL VIYDTSNLAS GVPARFSGSG
201 SGTSYSLTIS RMEAEDAATY YCQORDSYPL TFGAGTKLEL KRAATPVSEK
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301 QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351 LDLATYTAGG LPLQVPDEVT DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401 LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451 KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALLAQ
501 SRYWRIGSMY QGLGWEMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551 PVKASWVHKT GSTGGFGSYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601 LEALQ

Fig. 5A Amino acid sequence of CAB1.7 protein

SEQ ID NO: 9


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1  QVQLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWVRQG PEQGLEWIGW
51 IDPENGDT EY APKFQ GKATF TTDTS SNTAY LQLSSLTSED TAVYYCNEGL
101 PLGAIYNDYW GQGTTVTVSS GGGGSGGGGS GGGGSENVLT QSPAIVSASP
151 GEKVTITCSA SSAVYAMHWF QQKPGTSPKL VIYDTSNLAS GVPARFSGSG
201 SGTSYSLTIS RMEAEDAATY YCQQRDSYPL TFGAGTKLEL KRAATPVSEK
251 QLAEVVANTI TPLMAAQSV P GMAVAVIYQG KPHY YTFGKA DIAANKPVTP
301 QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351 LDLATYTAGG LPLQVPDEVT DNA'SLLRFYQ NWQPQWKPGT TRLYANASIG
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451 KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501 SRYWRIGSMY QGLGW EMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551 PVKASWVHKT GSTGGFGAYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601 LEALQ
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Fig. 5B Amino acid sequence of CAB1.7i protein

SEQ ID NO: 10

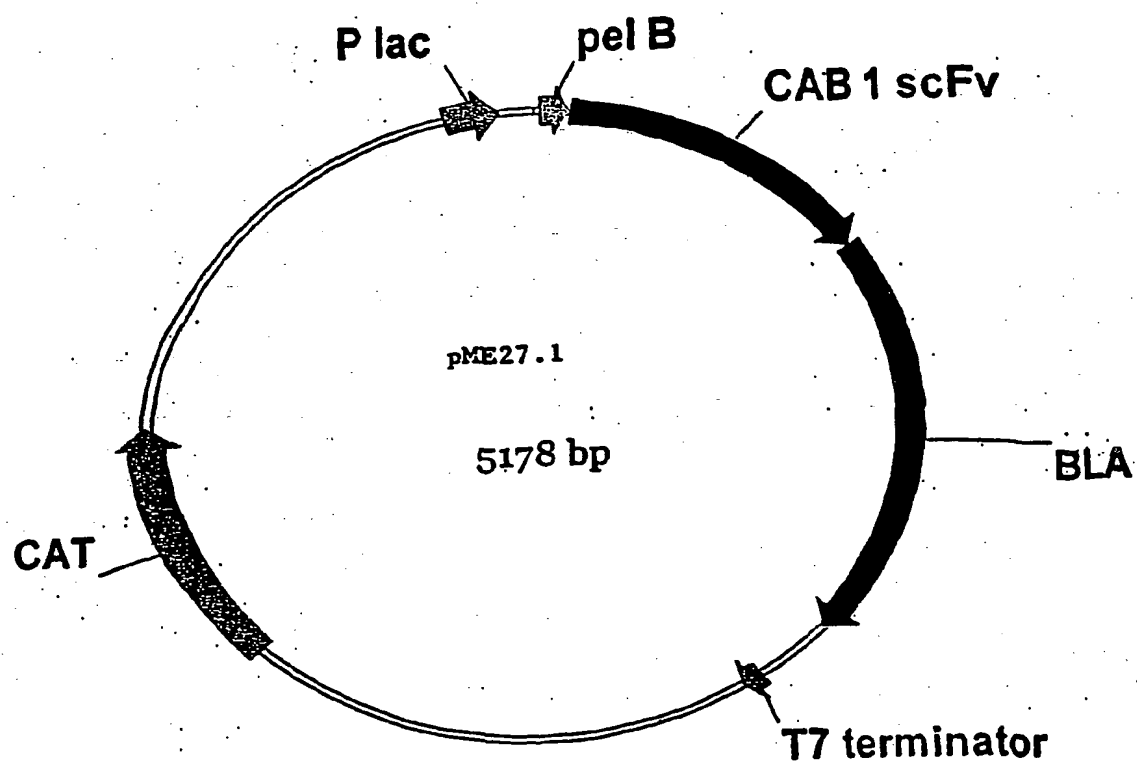


Figure 6A

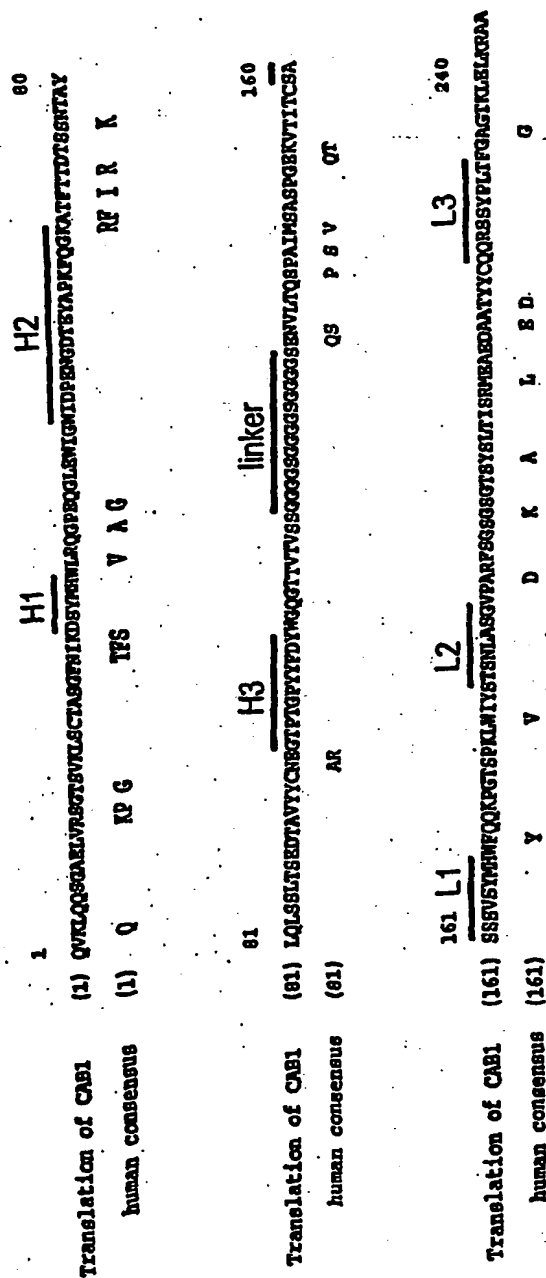


Figure 6B

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Figure 6C - 1

heavy chain:
qvklqqsgaelvrsqsvklscstasgfnikdsymhwlrqgpeqglewigwidpengdeyapkfgkafitidssntaylqlssltseidavyyccnegtpgpyyfdywgqggtvtvss

linker:
ggggsgggsgggsgs

light chain:
envltqspaimsaspgckvtitcsasssvsymhwlqqkpgtspklwiystsnlasgvpafsgsgsgtsysltisrmeaedaatyecqrrssypiltfgagtklelkraat

BLA:
pvsekqlaevvantiiplmkaqsvpgmavaiyqgkphyytfgkadiaankpvtpqlfelgsiskttfvlggdaiaargeisldavtrywpqltgkqwqgimldlatytagglpqlvpdevtd
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Figure 6D

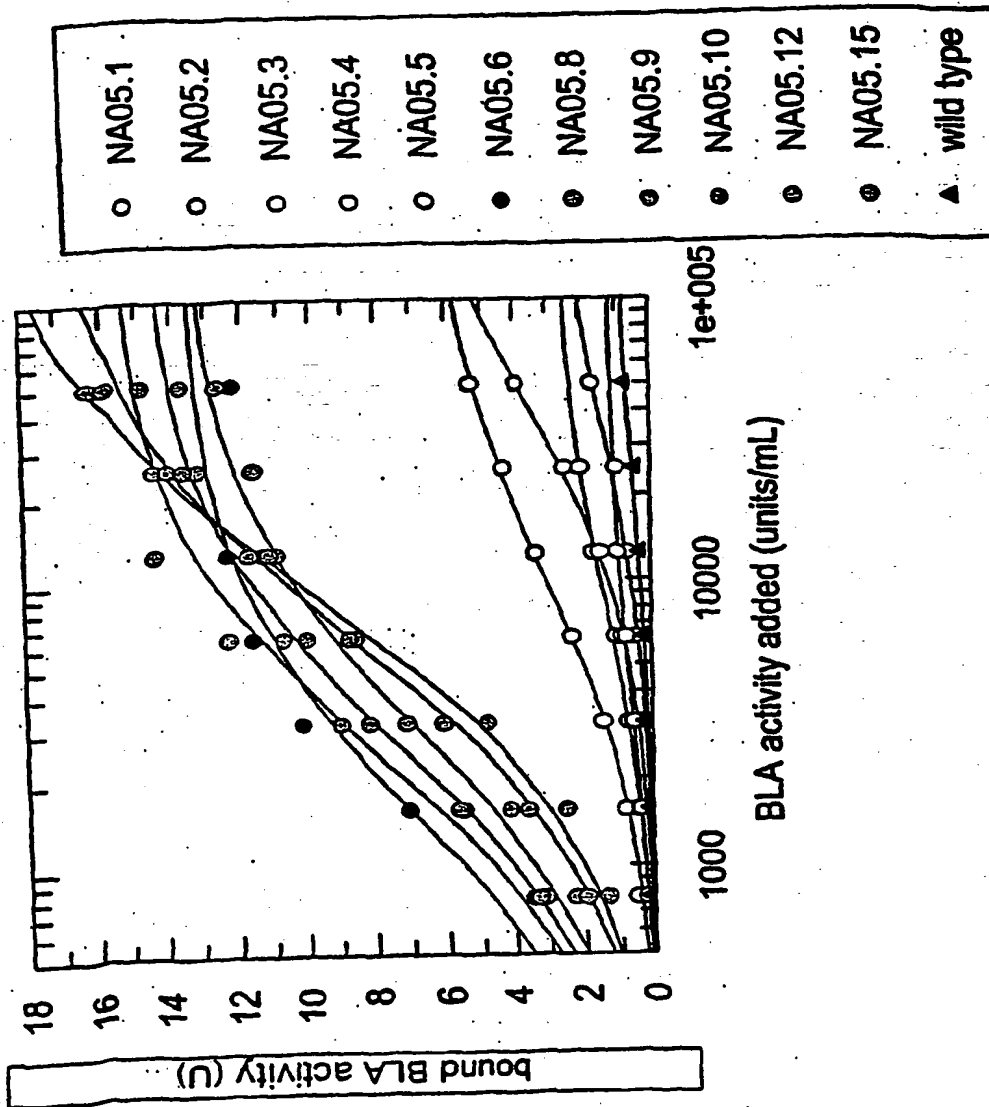


Figure 7A

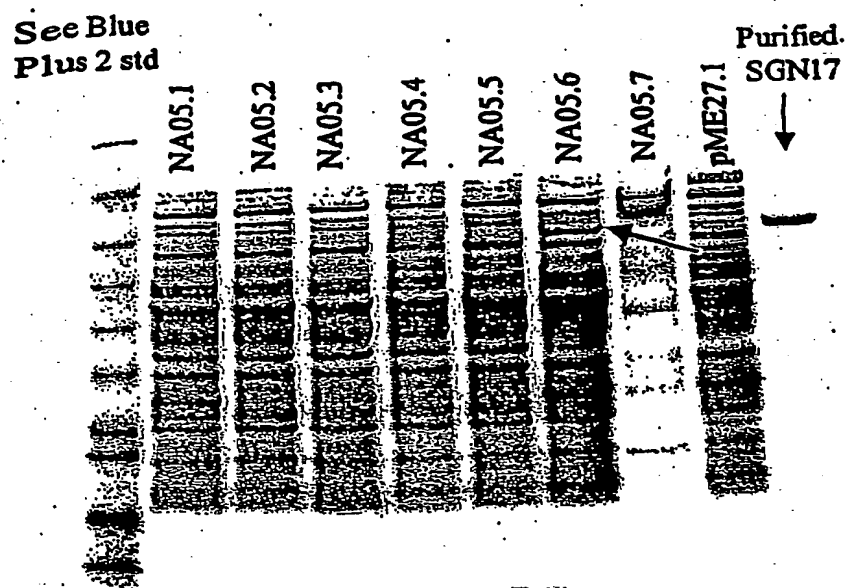


Figure 7B

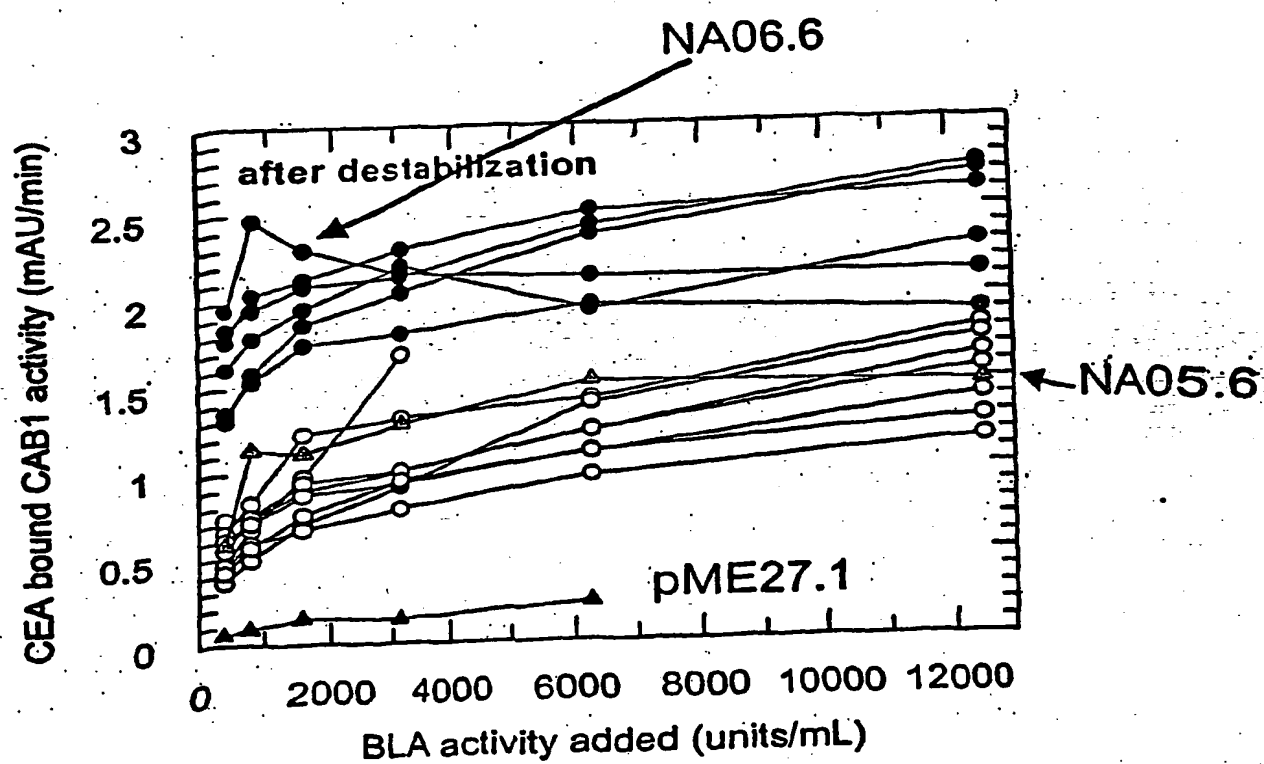


Figure 7C

pos. heavy chain	number of observations	observed frequencies of 5 most abundant amino acids in alignment of human sequences												CAB1 sequence	CDR	mutated residues
1	291	E	0.616	Q	0.346	D	0.014	G	0.014	A	0.003	L	0.003	Q		
2	293	V	0.887	M	0.027	L	0.024	S	0.020	I	0.017	A	0.007	V		
3	291	Q	0.852	H	0.034	R	0.027	T	0.027	E	0.014	V	0.014	K		1
4	282	L	0.975	V	0.011	A	0.007	D	0.004	M	0.004			L		
5	276	V	0.645	Q	0.148	L	0.120	R	0.022	M	0.014	N	0.014	Q		
6	267	E	0.693	Q	0.263	A	0.022	D	0.011	G	0.007	R	0.004	Q		
7	265	S	0.951	W	0.019	X	0.015	T	0.008	A	0.004	N	0.004	S		
8	266	G	0.989	S	0.008	T	0.004							G		
9	274	G	0.624	A	0.193	P	0.164	S	0.011	E	0.004	H	0.004	A		
10	271	G	0.638	E	0.192	D	0.081	A	0.070	T	0.011	V	0.007	E		
11	270	L	0.681	V	0.270	F	0.030	S	0.019					L		
12	267	V	0.757	K	0.154	I	0.026	N	0.022	L	0.015	A	0.007	V		
13	247	K	0.474	Q	0.428	R	0.049	E	0.034	G	0.004	H	0.004	R		1
14	251	P	0.968	A	0.012	K	0.008	G	0.004	L	0.004	S	0.004	S		1
15	244	G	0.783	S	0.156	T	0.033	P	0.016	K	0.008	E	0.004	G		
16	243	G	0.488	E	0.131	Q	0.107	A	0.094	R	0.082	S	0.066	T		1
17	234	S	0.766	T	0.204	A	0.009	F	0.009	P	0.004	R	0.004	S		
18	244	L	0.812	V	0.155	M	0.008	A	0.004	E	0.004	F	0.004	V		
19	242	R	0.545	K	0.240	S	0.161	T	0.037	A	0.012	Q	0.004	K		
20	246	L	0.736	V	0.191	I	0.061	E	0.004	R	0.004	X	0.004	L		
21	218	S	0.729	T	0.234	G	0.009	I	0.009	A	0.005	D	0.005	S		
22	217	C	0.991	R	0.005	S	0.005							C		
23	231	A	0.558	K	0.203	T	0.117	E	0.048	V	0.022	I	0.013	T		
24	235	A	0.638	V	0.174	G	0.064	I	0.055	T	0.030	F	0.026	A		
25	226	S	0.951	Y	0.027	F	0.009	C	0.004	K	0.004	T	0.004	S		
26	225	G	0.956	E	0.013	A	0.009	D	0.009	S	0.009	V	0.004	G		
27	213	F	0.559	Y	0.164	G	0.150	D	0.080	S	0.019	L	0.014	F		
28	203	T	0.571	S	0.286	I	0.049	N	0.049	P	0.015	A	0.005	N		1
29	207	F	0.749	V	0.111	I	0.068	L	0.053	T	0.010	A	0.005	I		1
30	202	S	0.762	T	0.119	N	0.035	G	0.020	R	0.020	A	0.010	K		1
31	199	S	0.482	T	0.136	D	0.104	N	0.087	G	0.060	K	0.040	D	H1	
32	202	Y	0.535	S	0.144	N	0.083	A	0.069	D	0.031	G	0.030	S	H1	
33	197	A	0.269	Y	0.162	G	0.147	W	0.117	S	0.091	T	0.066	Y	H1	
34	200	M	0.520	I	0.210	W	0.070	A	0.055	Y	0.050	V	0.040	M	H1	
35	196	S	0.372	H	0.235	N	0.077	A	0.061	G	0.051	Y	0.046	H	H1	
35a	33	-	0.824	W	0.096	V	0.043	G	0.016	S	0.016	N	0.005		H2	
35b	27	-	0.856	N	0.064	G	0.037	S	0.032	A	0.005	R	0.005		H3	
36	192	W	0.990	M	0.005	T	0.005							W		
37	193	V	0.741	I	0.228	L	0.021	G	0.005	Q	0.005			L		1
38	190	R	0.989	P	0.005	V	0.005							R		
39	190	Q	0.979	T	0.011	G	0.005	R	0.005					Q		
40	191	A	0.634	P	0.199	S	0.073	M	0.052	G	0.010	V	0.010	G		1
41	187	P	0.914	S	0.043	T	0.021	A	0.005	L	0.005	Q	0.005	P		
42	187	G	0.925	S	0.064	P	0.005	R	0.005					E		1
43	186	K	0.683	Q	0.183	R	0.124	E	0.005	H	0.005			Q		
44	186	G	0.882	A	0.048	S	0.043	R	0.027					G		
45	186	L	0.978	P	0.022									L		
46	185	E	0.956	Q	0.039	V	0.005							E		
47	184	W	0.989	S	0.011									W		

Figure 8A — 1

48	185	V	0.481	M	0.218	I	0.173	L	0.124	E	0.005	L	0.005	0.005	G		
49	185	G	0.600	S	0.218	A	0.162	E	0.105	L	0.005	G	0.081	Y	0.081	W	H2
50	185	R	0.146	W	0.146	V	0.119	A	0.114	G	0.081	Y	0.081	Y	0.081	W	H2
51	185	I	0.822	T	0.081	R	0.027	V	0.022	K	0.016	M	0.016	M	0.011	I	H2
52	184	S	0.250	Y	0.239	N	0.123	K	0.060	I	0.054	D	0.054	D	0.050	D	H2
52a	141	-	0.230	P	0.180	Y	0.153	G	0.126	N	0.066	V	0.066	V	0.055	P	H2
52b	34	-	0.814	K	0.115	R	0.060	G	0.005	Y	0.005						H2
52c	22	-	0.880	T	0.044	V	0.033	S	0.022	A	0.011	G	0.011	G	0.005		H2
53	184	S	0.228	D	0.163	Y	0.125	G	0.109	N	0.082	H	0.082	H	0.054	E	H2
54	183	G	0.328	S	0.202	D	0.129	N	0.112	K	0.082	F	0.082	F	0.055	N	H2
55	182	G	0.544	S	0.181	D	0.085	W	0.066	Y	0.060	N	0.060	N	0.020	G	H2
56	182	S	0.231	D	0.182	N	0.147	T	0.143	Y	0.077	G	0.077	G	0.060	D	H2
57	184	T	0.582	K	0.120	N	0.065	A	0.054	I	0.054	P	0.054	P	0.022	T	H2
58	183	Y	0.322	N	0.216	D	0.139	R	0.060	H	0.055	T	0.055	T	0.038	E	H2
59	184	Y	0.908	F	0.043	N	0.016	S	0.011	D	0.005	G	0.005	G	0.005	Y	H2
60	183	A	0.579	N	0.153	S	0.104	T	0.055	R	0.044	G	0.044	G	0.027	A	H2
61	184	D	0.277	P	0.239	Q	0.174	A	0.141	V	0.076	T	0.076	T	0.033	P	H2
62	185	S	0.686	K	0.146	F	0.065	N	0.038	G	0.016	R	0.016	R	0.016	K	H2
63	186	V	0.511	L	0.247	F	0.215	S	0.011	A	0.005	K	0.005	K	0.005	F	H2
64	186	K	0.581	Q	0.274	R	0.054	N	0.032	E	0.022	T	0.022	T	0.022	Q	H2
65	186	G	0.688	S	0.237	T	0.032	A	0.016	D	0.011	E	0.011	E	0.011	G	H2
66	186	R	0.935	Q	0.054	H	0.005	I	0.005							K	1
67	186	F	0.462	V	0.409	I	0.065	L	0.054	A	0.005	S	0.005	S	0.005	A	1
68	186	T	0.914	I	0.038	A	0.016	S	0.011	K	0.005	N	0.005	N	0.005	T	
69	187	I	0.791	M	0.139	V	0.032	D	0.005	F	0.005	G	0.005	G	0.005	F	1
70	187	S	0.684	T	0.214	N	0.070	L	0.032							T	
71	187	R	0.529	V	0.160	A	0.107	P	0.064	T	0.053	K	0.053	K	0.043	T	1
72	186	D	0.902	N	0.071	K	0.016	E	0.011							D	
73	185	T	0.368	N	0.266	D	0.177	K	0.070	E	0.059	A	0.059	A	0.011	T	
74	186	S	0.946	A	0.048	L	0.005									S	
75	187	K	0.674	T	0.139	I	0.070	R	0.027	A	0.021	F	0.021	F	0.021	S	1
76	187	N	0.701	S	0.251	K	0.027	R	0.011	T	0.005	Y	0.005	Y	0.005	N	
77	187	T	0.615	Q	0.273	S	0.048	M	0.021	L	0.016	P	0.016	P	0.011	T	
78	186	L	0.364	A	0.273	F	0.235	V	0.096	I	0.005	M	0.005	M	0.005	A	
79	187	Y	0.638	S	0.239	F	0.059	V	0.048	H	0.005	M	0.005	M	0.005	Y	
80	187	L	0.782	M	0.207	N	0.005	-	0.005							L	
81	187	Q	0.529	E	0.205	K	0.122	R	0.032	T	0.032	N	0.032	N	0.027	Q	
82	194	M	0.497	L	0.421	W	0.051	V	0.015	I	0.010	-	0.010	-	0.005	L	
82a	195	N	0.442	S	0.291	R	0.077	T	0.066	D	0.053	G	0.053	G	0.020	S	
82b	194	S	0.795	N	0.082	R	0.051	G	0.026	T	0.021	A	0.021	A	0.010	S	
82c	197	L	0.701	V	0.234	M	0.041	G	0.010	A	0.005	D	0.005	D	0.005	L	
83	197	R	0.528	T	0.239	K	0.122	D	0.041	E	0.020	Q	0.020	Q	0.015	T	
84	198	A	0.495	P	0.182	S	0.177	T	0.051	I	0.035	V	0.035	V	0.030	S	
85	198	E	0.591	A	0.172	D	0.126	S	0.051	V	0.045	G	0.045	G	0.015	E	
86	198	D	0.975	T	0.010	V	0.010	N	0.005							D	
87	198	T	0.929	S	0.035	G	0.010	M	0.010	A	0.005	Q	0.005	Q	0.005	T	
88	198	A	0.939	G	0.040	P	0.005	T	0.005	V	0.005	Y	0.005	Y	0.005	A	
89	198	V	0.768	L	0.066	M	0.056	T	0.045	I	0.040	F	0.040	F	0.010	V	
90	199	Y	0.980	F	0.010	A	0.005	I	0.005							Y	
91	199	Y	0.930	F	0.045	C	0.015	R	0.005	T	0.005					Y	
92	198	C	0.990	A	0.005	M	0.005									C	
93	198	A	0.838	T	0.076	V	0.061	H	0.005	K	0.005	N	0.005	N	0.005	N	1
94	198	R	0.596	K	0.162	T	0.051	G	0.045	P	0.045	Q	0.045	Q	0.025	E	1
95	161	G	0.174	D	0.120	E	0.099	A	0.093	N	0.092	P	0.092	P	0.068	G	
96	159	P	0.168	R	0.130	G	0.112	L	0.062	V	0.062	Y	0.062	Y	0.062	T	H3
97	156	G	0.170	P	0.094	V	0.094	E	0.088	T	0.069	S	0.069	S	0.063	P	H3
98	155	G	0.162	Y	0.101	L	0.095	D	0.087	V	0.076	S	0.076	S	0.063	T	H3

pos. light chain	number of observations	observed frequencies of 5 most abundant amino acids in alignment of human sequences													CAB1 sequence	CDR	mutated residues
		Q	S	N	H	D	F	E	T	V	L	I	K	P			
1	95	Q	0.589	S	0.158	N	0.095	H	0.074	D	0.053	F	0.021	E			1
2	139	S	0.446	Y	0.388	F	0.101	V	0.043	L	0.014	T	0.007	N			1
3	140	V	0.307	E	0.243	A	0.207	M	0.093	D	0.064	I	0.043	V			
4	140	L	0.971	V	0.029									L			
5	141	T	0.915	A	0.021	S	0.021	I	0.014	K	0.007	L	0.007	T			
6	140	Q	0.993	E	0.007									Q			
7	139	P	0.906	D	0.029	S	0.029	A	0.022	E	0.014			S			1
8	139	P	0.741	A	0.137	H	0.072	R	0.029	L	0.007	S	0.007	P			1
9	139	S	0.964	A	0.014	V	0.014	R	0.007					A			1
10	0	-	1.000											I			1
11	138	V	0.790	A	0.138	L	0.058	M	0.014					M			1
12	139	S	0.978	F	0.007	T	0.007	E	0.004	Q	0.004			S			
13	138	V	0.406	G	0.348	A	0.138	E	0.087	L	0.014	D	0.007	A			
14	135	S	0.630	A	0.230	T	0.111	D	0.007	F	0.007	G	0.007	S			
15	135	P	0.881	L	0.089	A	0.022	S	0.007					P			
16	134	G	0.978	E	0.015	L	0.007							G			
17	133	Q	0.811	K	0.098	A	0.045	E	0.024	G	0.015	H	0.008	E			1
18	133	T	0.504	S	0.263	R	0.135	K	0.068	E	0.008	G	0.008	K			1
19	130	V	0.454	A	0.385	I	0.146	G	0.008	L	0.008			V			
20	128	T	0.531	R	0.188	S	0.148	K	0.047	I	0.031	M	0.016	T			
21	121	I	0.901	V	0.050	L	0.017	A	0.008	F	0.008	M	0.008	I			
22	120	S	0.492	T	0.475	A	0.008	G	0.008	I	0.008	N	0.008	T			
23	117	C	1.000											C			
24	112	S	0.536	T	0.259	G	0.089	A	0.045	Q	0.033	I	0.018	S	L1		
25	108	G	0.870	L	0.056	R	0.028	A	0.019	I	0.009	P	0.009	A	L1		
26	108	D	0.339	S	0.250	T	0.213	N	0.087	E	0.037	G	0.037	S	L1		
27	104	S	0.415	N	0.118	K	0.113	A	0.104	T	0.066	G	0.047	S	L1		
28	104	L	0.346	S	0.346	I	0.115	G	0.067	A	0.058	D	0.019	S	L1		
29	100	G	0.243	N	0.239	D	0.159	S	0.078	P	0.068	H	0.058	V	L1		
30	103	I	0.291	V	0.165	D	0.136	N	0.107	E	0.058	S	0.049	S	L1		
31	101	G	0.356	K	0.168	A	0.099	E	0.084	Q	0.084	D	0.069	Y	L1		
31a	54	-	0.438	S	0.167	G	0.104	N	0.083	Y	0.063	D	0.052	M	L1		
31b	49	-	0.495	N	0.227	Y	0.155	S	0.041	G	0.021	H	0.021	H	L1		
31c	23	-	0.760	N	0.134	S	0.031	K	0.021	D	0.012	E	0.010		L1		
31d	0	-	1.000												L1		
31e	0	-	1.000												L1		
31f	0	-	1.000												L1		
32	94	Y	0.515	S	0.134	F	0.093	A	0.072	T	0.052	H	0.041				
33	97	V	0.680	A	0.186	I	0.082	Y	0.021	F	0.010	P	0.010				
34	92	S	0.380	H	0.120	A	0.109	Y	0.098	N	0.076	Q	0.076				
35	98	W	0.990	Y	0.010									W			
36	96	Y	0.844	F	0.073	H	0.073	W	0.010					F			1
37	95	Q	0.916	R	0.042	E	0.011	H	0.011	K	0.011	Y	0.011	Q			
38	94	Q	0.862	H	0.053	L	0.053	E	0.011	K	0.011	V	0.011	Q			
39	93	K	0.333	L	0.172	R	0.161	H	0.151	Q	0.088	V	0.043	K			
40	93	P	0.946	S	0.022	A	0.011	L	0.011	R	0.011			P			

Figure 8B - 1

41	93	G	0.871	H	D	0.022	R	0.022	P	0.011	G			
42	92	Q	0.424	T	0.217	K	0.163	R	0.087	S	0.011	V	0.022	T
43	92	A	0.717	S	0.174	G	0.065	T	0.022	L	0.011		0.011	S
44	93	P	0.978	A	0.011	M	0.011							P
45	92	K	0.391	V	0.315	R	0.109	L	0.065	T	0.065	A	0.033	K
46	92	L	0.728	V	0.076	F	0.065	T	0.043	A	0.022	M	0.022	L
47	91	V	0.484	L	0.374	I	0.077	M	0.055	N	0.011			W
48	91	I	0.791	V	0.110	M	0.077	L	0.011	S	0.011			I
49	91	Y	0.769	F	0.110	R	0.066	H	0.022	D	0.011	I	0.011	Y
50	89	D	0.303	E	0.210	Q	0.093	V	0.067	G	0.056	K	0.056	S
51	88	D	0.364	N	0.205	V	0.159	H	0.068	T	0.068	G	0.034	T
52	89	N	0.393	T	0.213	S	0.202	D	0.101	A	0.022	F	0.011	S
53	88	K	0.307	D	0.193	Q	0.182	N	0.080	E	0.057	S	0.057	N
54	88	R	0.875	X	0.068	K	0.034	L	0.011	W	0.011			L
55	86	P	0.851	G	0.080	S	0.023	A	0.011	H	0.011	R	0.011	A
56	85	S	0.837	D	0.081	P	0.023	A	0.012	L	0.012	T	0.012	S
57	86	G	0.920	E	0.034	S	0.011	T	0.011	W	0.011	-	0.011	G
58	84	I	0.600	V	0.353	A	0.012	G	0.012	T	0.012	-	0.012	V
59	84	P	0.847	S	0.106	A	0.012	L	0.012	V	0.012	-	0.012	P
60	85	D	0.488	E	0.325	N	0.047	A	0.035	H	0.023	L	0.023	A
61	87	R	0.977	D	0.011	-	0.011							R
62	88	F	0.943	I	0.034	L	0.011	R	0.011					F
63	87	S	0.989	F	0.011									S
64	87	G	0.885	A	0.069	S	0.023	V	0.023					G
65	87	S	0.977	G	0.011	Y	0.011							S
66	86	K	0.430	N	0.186	S	0.186	T	0.081	X	0.070	R	0.035	G
67	85	S	0.953	T	0.024	K	0.012	L	0.012					S
68	85	G	0.859	S	0.071	A	0.035	D	0.024	Q	0.012			G
69	85	N	0.434	T	0.318	A	0.129	D	0.036	G	0.024	K	0.024	T
70	85	T	0.529	S	0.341	E	0.082	A	0.024	K	0.024			S
71	85	A	0.847	R	0.082	V	0.059	S	0.012					Y
72	85	T	0.447	S	0.424	Y	0.082	A	0.035	I	0.012			S
73	85	L	0.988	S	0.012									L
74	85	T	0.706	A	0.165	G	0.106	I	0.012	L	0.012			T
75	85	I	0.929	V	0.047	A	0.012	L	0.012					I
76	85	S	0.718	T	0.200	N	0.035	I	0.024	G	0.012	R	0.012	S
77	85	G	0.765	R	0.129	S	0.094	E	0.012					R
78	85	L	0.588	V	0.224	T	0.106	A	0.071	G	0.012			M
79	85	Q	0.659	E	0.153	R	0.071	K	0.047	L	0.024	A	0.012	E
80	85	A	0.459	S	0.235	T	0.200	V	0.047	P	0.035	N	0.012	A
81	85	E	0.541	G	0.235	M	0.071	D	0.047	L	0.024	N	0.024	E
82	85	D	0.964	N	0.024	E	0.012							D
83	85	E	0.976	D	0.012	T	0.012							A
84	85	A	0.941	T	0.035	E	0.012	S	0.012					A
85	85	D	0.859	E	0.082	H	0.024	A	0.012	I	0.012	M	0.012	T
86	85	Y	0.976	F	0.012	H	0.012							Y
87	85	Y	0.894	F	0.106									Y
88	85	C	0.988	H	0.012									C
89	85	Q	0.482	A	0.153	S	0.141	G	0.094	C	0.059	N	0.035	Q
90	85	S	0.388	T	0.271	A	0.212	V	0.118	L	0.012			Q
91	85	W	0.576	Y	0.247	A	0.059	F	0.035	R	0.035	D	0.012	R
92	84	D	0.606	G	0.095	A	0.071	N	0.061	T	0.048	E	0.024	S
93	84	S	0.405	D	0.179	G	0.107	N	0.095	P	0.071	T	0.060	S
94	84	S	0.536	G	0.155	N	0.073	R	0.060	D	0.058	T	0.048	Y
95	82	S	0.265	L	0.253	G	0.108	N	0.096	T	0.084	A	0.036	P

Figure 8B - 2

95a	60	-	0.268	S	0.183	D	0.159	N	0.110	T	0.073	Q	0.049	L	L3	
95b	40	-	0.512	A	0.098	G	0.098	H	0.085	E	0.049	R	0.037	T	L3	
95c	5	-	0.939	P	0.037	A	0.012	G	0.012						L3	
95d	1	-	0.988	G	0.012										L3	
95e	0	-	1.000												L3	
95f	0	-	1.000												L3	
96	80	V	0.305	G	0.098	P	0.098	W	0.098	A	0.073	N	0.073		L3	
97	85	V	0.788	I	0.118	L	0.047	M	0.035	G	0.012			F		
98	86	F	0.988	V	0.012									G		
99	89	G	0.989	F	0.011									A		1
100	89	G	0.831	T	0.124	A	0.022	S	0.022					G		
101	89	G	1.000											T		
102	89	T	0.989	G	0.011											
103	88	K	0.739	N	0.091	R	0.068	Q	0.034	T	0.034	E	0.011	K		
104	87	L	0.667	V	0.322	Q	0.011							L		1
105	87	T	0.954	S	0.023	I	0.011	L	0.011					L		1
106	85	V	0.988	T	0.012									K		1
106a	84	L	0.952	V	0.024	P	0.012	Q	0.012					R		1
107	78	G	0.782	S	0.103	R	0.090	C	0.013	L	0.013			A		1
108	46	Q	0.957	P	0.022	R	0.022							A		1
109	46	P	0.957	K	0.022	Q	0.022									

Figure 8B - 3

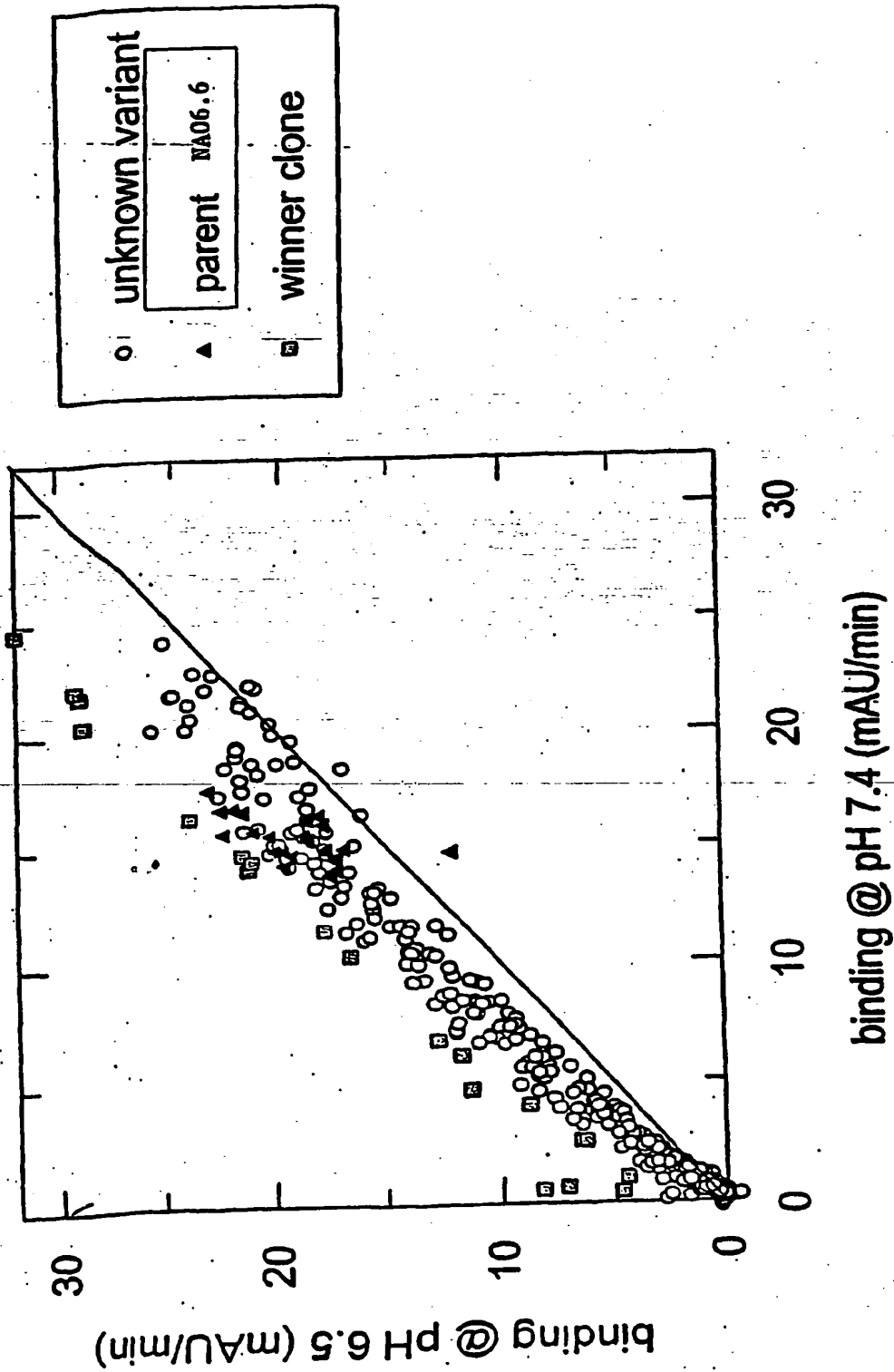


Figure 9

Residues chosen for
mutagenesis in NA06.6

CDRs in NA06.6

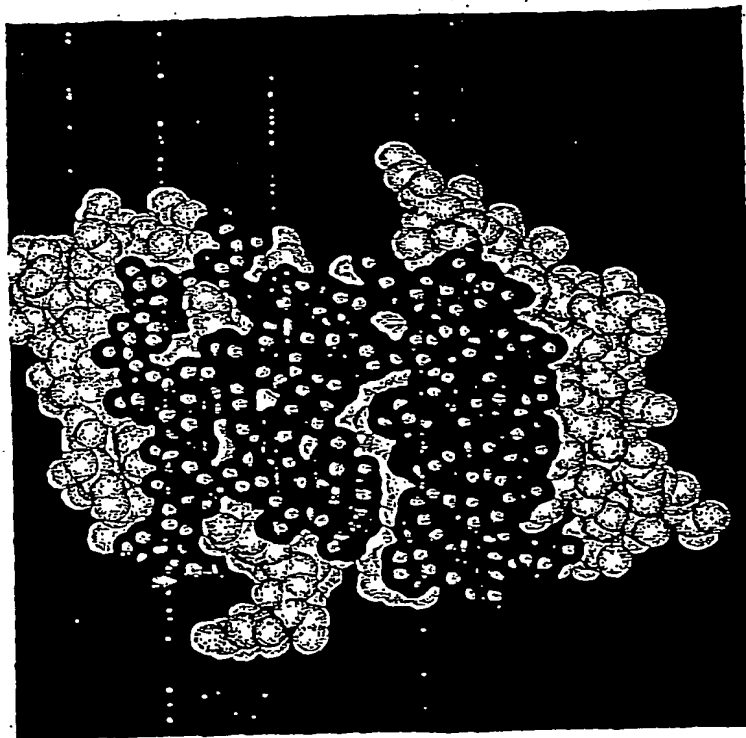
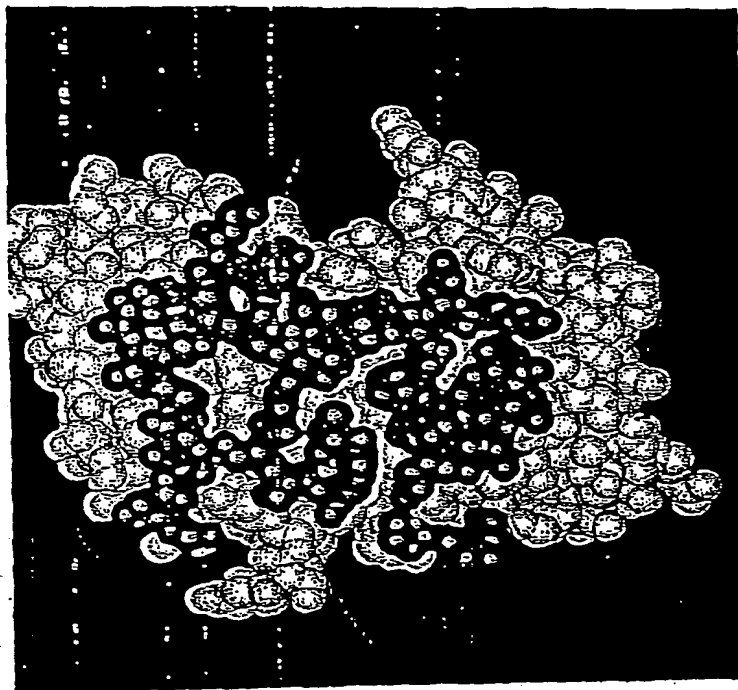


Figure 10

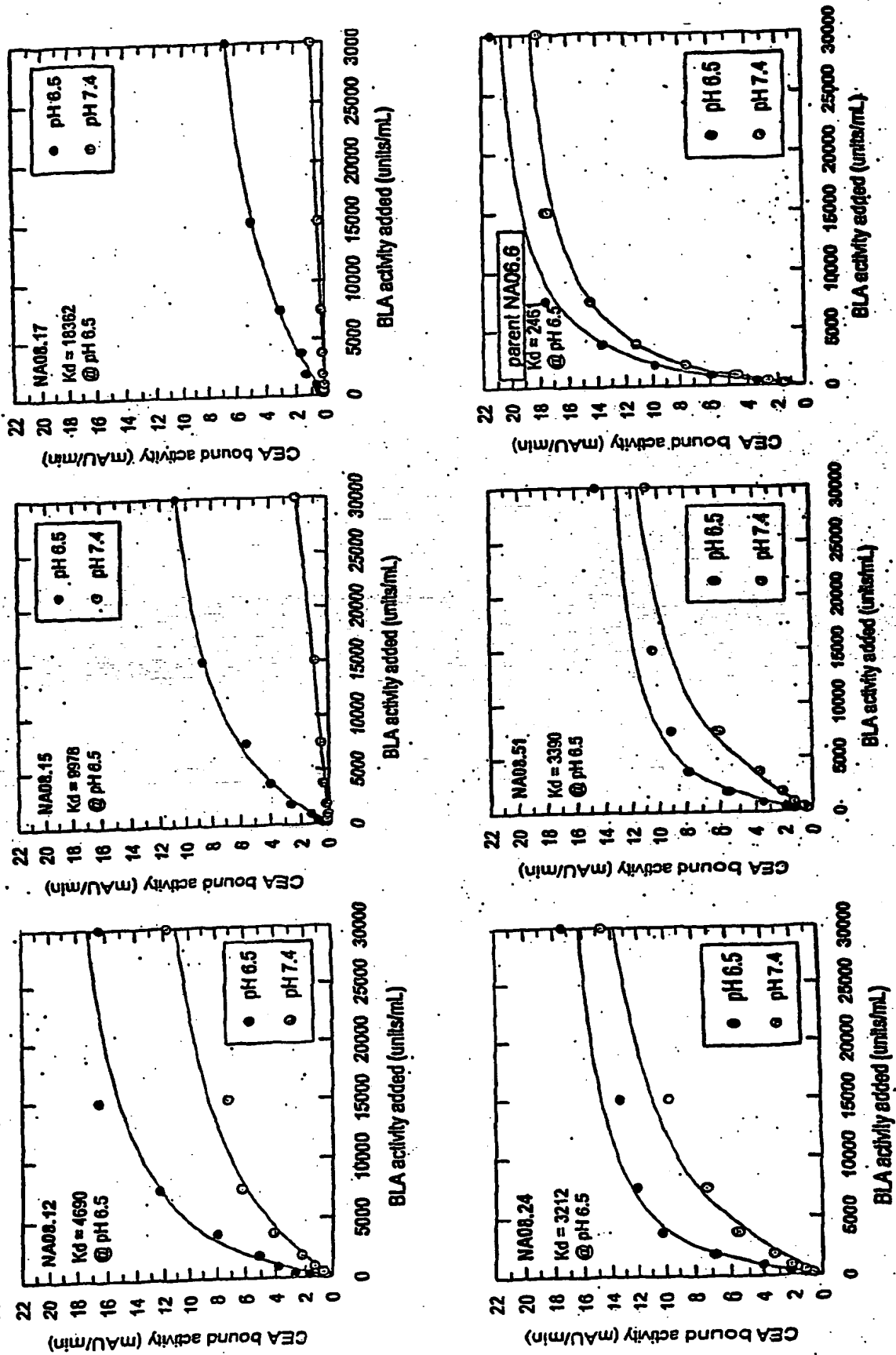


Figure 11

Figure 12: CAB1 engineering - summary

protein	changes	comments
CAB1	parent	
CAB1.1(NA05.6)	R13K, T16G, W181V	increase stability
CAB1.2(NA06.6)	K3Q, L37V, M146V	increase stability
CAB1.4(NA08.15)	S184D, S226D	pH-dependent binding
CAB1.6	T100L	increased affinity
SW149.5	T102L, P104A, Y105I, F107N	increased affinity
CAB1.7	S163T, S165Y, Y166S	increased affinity
CAB1.7i	in BLA: K265A, S568A	remove T-cell epitopes

cumulative changes
→

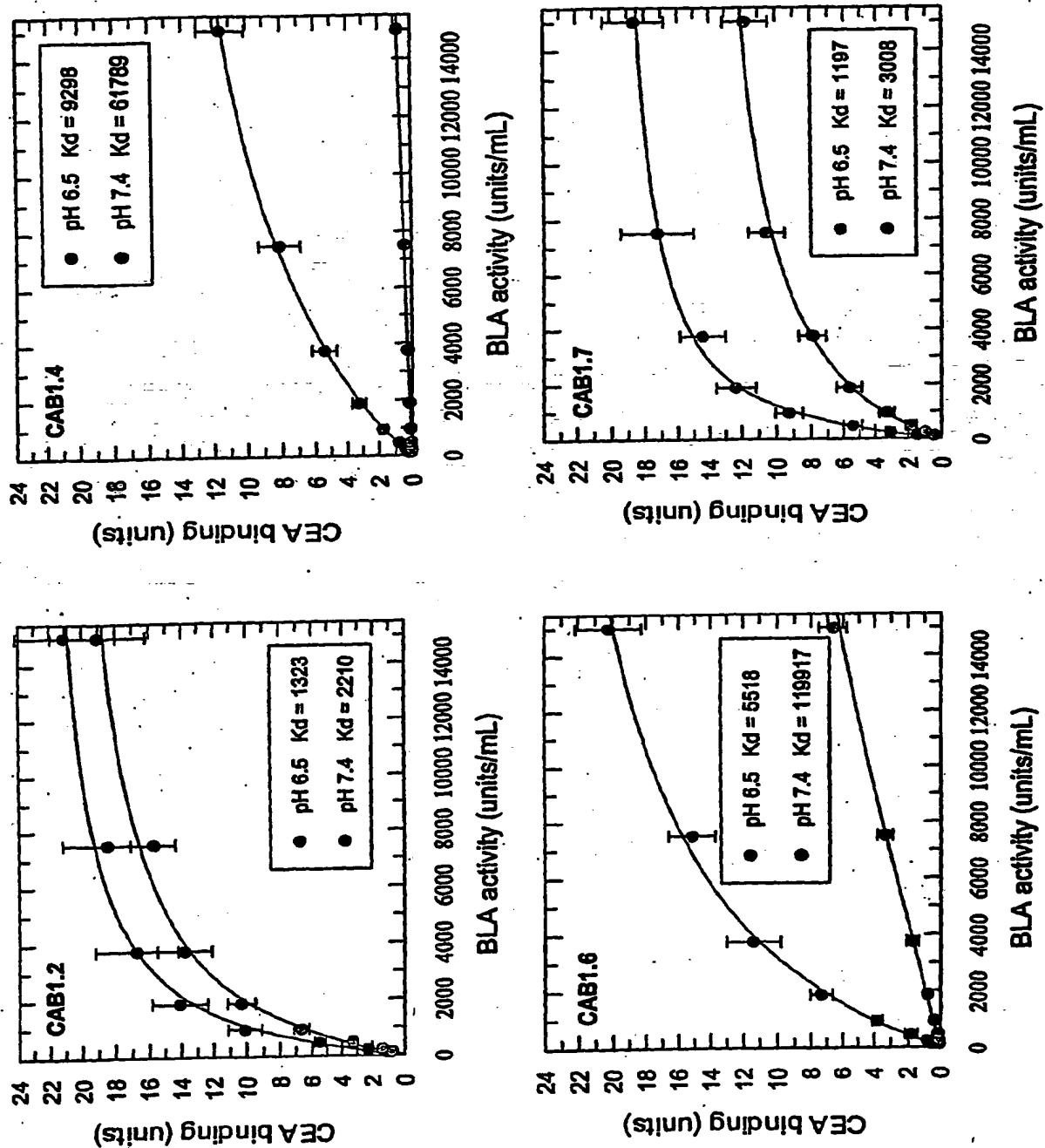
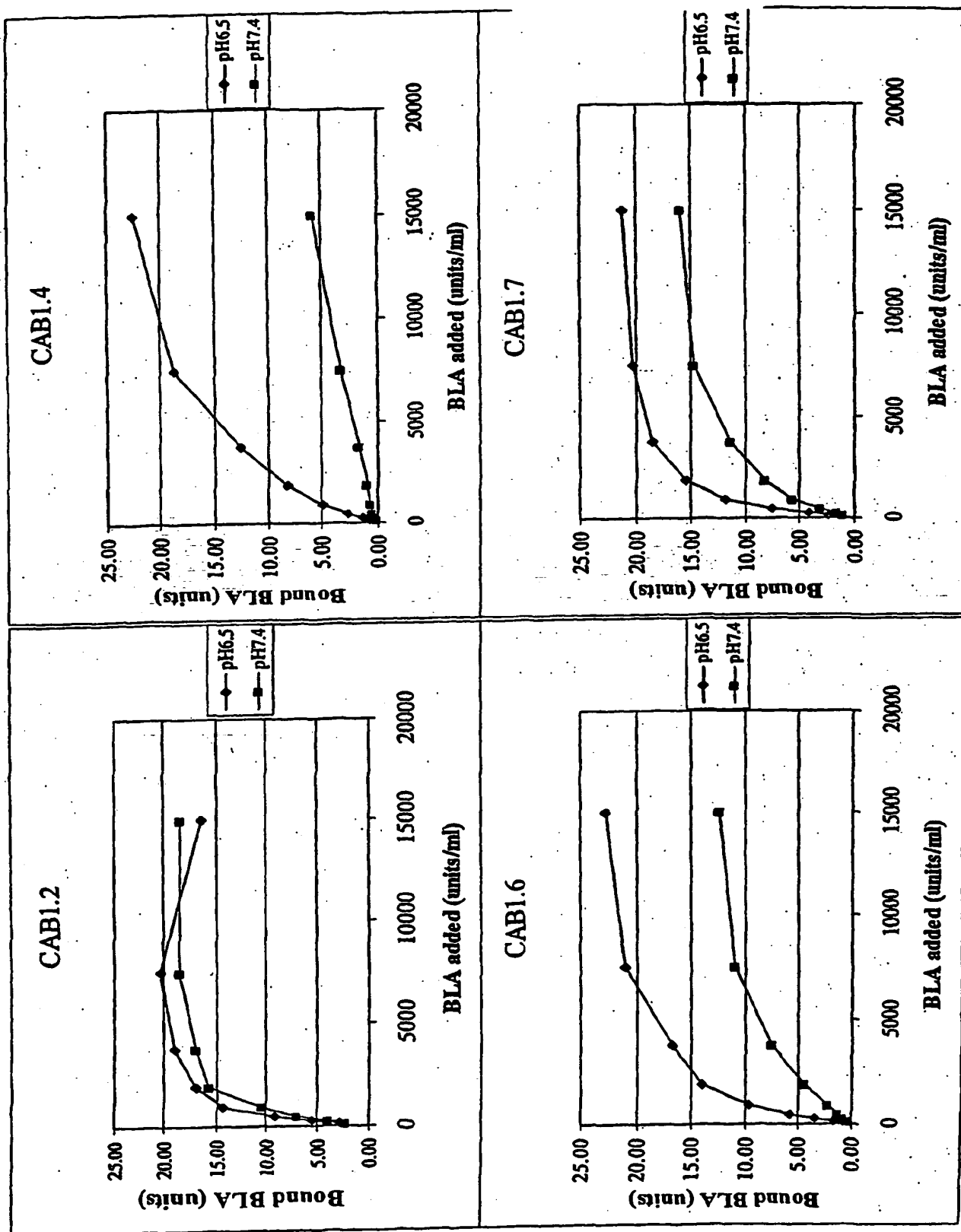
Figure 13: Binding of various CAB1 variants to immobilized CEA

Figure 14: Binding of various CAB1 variants to LS174T cells

1	QVQLQQSGAE	LVKSGGSVKL	SCTASGFNIK	DSYMHWVRQG	PEQGLEWIGW
51	IDPENGDTIEY	APKFQ GKATF	TTDTSSNTAY	LQLSSLTSED	TAVYYCNEGL
101	PLGAIYNDYW	GQGTTVTVSS	GGGGSGGGGS	GGGGSENVLT	QSPAIVSASP
151	GEKVTITCSA	SSSVSYMHWF	QQKPGTSPKL	VIYDTSNLAS	GVPARFSGSG
201	SGTSYSLTIS	RMEAEDAATY	YCQQRDSYPL	TFGAGTKLEL	KRAATPVSEK
251	QLAEVVANTI	TPLMKAQSV	GMAVAVIYQG	KPHYTYFGKA	DIAANKPVTP
301	QTLFELGSIS	KTFTGVLGGD	AIARGEISLD	DAVTRYWPQL	TGKQWQGIRM
351	LDLATYTAGG	LPLQVPDEVT	DNASLLRFYQ	NWQPQWKPGT	TRLYANASIG
401	LFGALAVKPS	GMPYEQAMTT	RVLKPLKLDH	TWINVPKAE	AHYAWGYRDG
451	KAVRVSPGML	DAQAYGVKTN	VQDMANWVMA	NMAPENVADA	SLKQGIALAQ
501	SRYWRIGSMY	QGLGWEMLNW	PVEANTTVET	SFGNVALAPL	PVAEVNPPAP
551	PVKASWVHKT	GSTGGFGSYV	AFIPEKQIGI	VMLANTSYPN	PARVEAAYHI
601	LEALQ				

Fig. 15A Amino acid sequence of SW149.5 protein

1	QVKLQQSGAE	LVKSGGSVKL	SCTASGFNIK	DSYMHWLRQG	PEOGLEWIGW
51	IDPENGDT	APKFQ GKATF	TTDTSSNTAY	LQLSSLTSED	TAVYYCNEGT
101	PTGPYYFDYW	GQGTTVTVSS	GGGGSGGGGS	GGGGSENVLT	QSPAIMSASP
151	GEKVTITCSA	SSSVSYMHWF	QOKPGTSPKL	VIYSTSNLAS	GVPARFSGSG
201	SGTSYSLTIS	RMEAEDAATY	YCQQRSSYPL	TFGAGTKLEL	KRAATPVSEK
251	QLAEVVANTI	TPLMKAQSV	GMAVAVIYQG	KPHYTTFGKA	DIAANKPVTP
301	QTLFELGSIS	KTFTGVLGGD	AIARGEISLD	DAVTRYWPQL	TGKQWQGIRM
351	LDLATYTAGG	LPLQVPDEVT	DNASLLRFYQ	NWQPQWKPGT	TRLYANASIG
401	LFGALAVKPS	GMPYEQAMTT	RVLKPLKLDH	TWINVPKAE	AHYAWGYRDG
451	KAVRVSPGML	DAQAYGVKTN	VQDMANWVMA	NMAPENVADA	SLKQGI
501	SRYWRIGSMY	QGLGWEMLNW	PVEANTVVET	SFGNVALAPL	PVAEVNPPAP
551	PVKASWVHKT	GSTGGFGSYV	AFIPEKQIGI	VMLANTSYPN	PARVEAAYHI
601	LEALQ				

Fig. 15B Amino acid sequence of CAB1.1 protein

```
1 CAGGTGCAGC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGGCTC
51 AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
101 TGCAGTGGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCGAAGT TCCAGGGCAA
201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGACT
301 CCGACTGGGC CGTACTACTT TGA TACTACTGG GGCCAAGGGA CCACGGTCAC
351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GGC GGTGGCG
401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCGTGTC TGCATCTCCA
451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAAGTG TAAGTTACAT
501 GCACTGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAAGTC GTGATTTATA
551 GCACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651 TGCCACTTAT TACTGCCAGC AAAGATCTAG TTACCCACTC ACGTTCGGTG
701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751 CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCCGCTGA TGAAAGCCCA
801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATCATG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTTATCAA AACTGGCAGC
1151 CGCAGTGGAA GCCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGTCATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GGCATATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTCGAGACG AGTTTTGGTA
1601 ATGTAGCACT GCGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CAGCTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG
```

Fig. 15C Nucleotide sequence of CAB1.2 gene

1	QVQLQQSGAE	LVKSGGSVKL	SCTASGFNIK	DSYMHWVRQG	PEQGLEWIGW
51	IDPENGDTFY	APKFQ GKATF	TTDTSSNTAY	LQLSSLTSED	TAVYYCNEG
101	PTGPYYFDYW	GQGT TVTVSS	GGGSGGGGS	GGGSENVLT	QSPAIVSASP
151	GEKVTITCSA	SSSVSYMHWF	QOKPGTSPKL	VIYSTSNLAS	GVPARFSGSG
201	SGTSYSLTIS	RMEAEDAATY	YCQQRSSYPL	TFGAGTKLEL	KRAATPVSEK
251	QLAEVVANTI	TPLMKAQSV	GMAVAVIYQG	KPHYTTFGKA	DIAANKPVTP
301	QTLFELGSIS	KTFTGVLGGD	AIARGEISLD	DAVTRYWPQL	TGKQWQGIRM
351	LDLATYTAGG	LPLQVPDEVT	DNASLLRFYQ	NWQPQWKPGT	TRLYANASIG
401	LFGALAVKPS	GMPYEQAMTT	RVLKPLKLDH	TWINVPKAE	AHYAWGYRDG
451	KAVRVSPGML	DAQAYGVKTN	VQDMANWVMA	NMAPENVADA	SLKQGIALAQ
501	SRYWRIGSMY	QGLGWEMLNW	PVEANTVVET	SFGNVALAPL	PVAEVNPPAP
551	PVKASWVHKT	GSTGGFGSYV	AFIPEKQIGI	VMLANTSYPN	PARVEAAYHI
601	LEALQ				

Fig. 15D Amino acid sequence of CAB1.2 protein

H1CDR (26) GFNIKDSYMH (35)
H2CDR (50) WIDPENGDTHEYAPKFQ (65)
H3CDR (99) GTPTGPYYFDY (109)
L1CDR (159) SASSSVSYMH (168)
L2CDR (184) DTSNLAS (190)
L3CDR (223) QQRDSYPLT (231)

Fig. 15E Amino acid sequences of CAB1.4 CDRs

H1CDR (154) GGCTTCAACATTAAAGACTCCTATATGCAC (183)

H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCCAG (273)

H3CDR (373) GGGACTCCGACTGGGCCGTACTACTTTGACTAC (405)

L1CDR (553) AGTGCCAGCTCAAGTGTAAGTTACATGCAC (582)

L2CDR (628) GATACATCCAACCTGGCTTCT (648)

L3CDR (745) CAGCAAAGAGATAGTTACCCACTCAG (771)

Fig. 15F Nucleotide sequence of CAB1.4 CDRs

```
1  CAGGTGCAGC  TGCAGCAGTC  TGGGGCAGAA  CTTGTGAAAT  CAGGGGGGCTC
51  AGTCAAGTTG  TCCTGCACAG  CTTCTGGCTT  CAACATTAAA  GACTCCTATA
101 TGCACCTGGT  GAGGCAGGGG  CCTGAACAGG  GCCTGGAGTG  GATTGGATGG
151 ATTGATCCTG  AGAATGGTGA  TACTGAATAT  GCCCCGAAGT  TCCAGGGCAA
201 GGCCACTTTT  ACTACAGACA  CATCCTCCAA  CACAGCCTAC  CTGCAGCTCA
251 GCAGCCTGAC  ATCTGAGGAC  ACTGCCGTCT  ATTATTGTAA  TGAGGGGACT
301 CCGACTGGGC  CGTACTACTT  TGACTACTGG  GGCCAAGGGA  CCACGGTCAC
351 CGTCTCCTCA  GGTGGAGGCG  GTTCAGGCGG  AGGTGGCTCT  GGCGGTGGCG
401 GATCAGAAAA  TGTGCTCACC  CAGTCTCCAG  CAATCGTGTC  TGCATCTCCA
451 GGGGAGAAGG  TCACCATAAC  CTGCAGTGCC  AGCTCAAGTG  TAAGTTACAT
501 GCACTGGTTC  CAGCAGAAGC  CAGGCACTTC  TCCCAAATC  GTGATTTATG
551 ATACATCCAA  CCTGGCTTCT  GGAGTCCCTG  CTCGCTTCAG  TGGCAGTGGA
601 TCTGGGACCT  CTTACTCTCT  CACAATCAGC  CGAATGGAGG  CTGAAGATGC
651 TGCCACTTAT  TACTGCCAGC  AAAGAGATAG  TTACCCACTC  ACGTTCGGTG
701 CTGGCACCAA  GCTGGAGCTG  AAACGGGCGG  CCACACCGGT  GTCAGAAAAA
751 CAGCTGGCGG  AGGTGGTCGG  GAATACGATT  ACCCCGCTGA  TGAAAGCCCA
801 GTCTGTTCCA  GGCATGGCGG  TGGCCGTTAT  TTATCAGGGA  AAACCGCACT
851 ATTACACATT  TGGCAAGGCC  GATATCGCGG  CGAATAAACC  CGTTACGCCT
901 CAGACCCTGT  TCGAGCTGGG  TTCTATAAGT  AAAACCTTCA  CCGGCGTTTT
951 AGGTGGGGAT  GCCATTGCTC  GCGGTGAAAT  TTCGCTGGAC  GATGCGGTGA
1001 CCAGATACTG  GCCACAGCTG  ACGGGCAAGC  AGTGGCAGGG  TATTCGTATG
1051 CTGGATCTCG  CCACCTACAC  CGCTGGCGGC  CTGCCGCTAC  AGGTACCGGA
1101 TGAGGTCACG  GATAACGCCT  CCCTGCTGCG  CTTTTATCAA  AACTGGCAGC
1151 CGCAGTGGA  GCCTGGCACA  ACGCGTCTTT  ACGCCAACGC  CAGCATCGGT
1201 CTTTTTGGTG  CGCTGGCGGT  CAAACCTTCT  GGCATGCCCT  ATGAGCAGGC
1251 CATGACGACG  CGGGTCCTTA  AGCCGCTCAA  GCTGGACCAT  ACCTGGATTA
1301 ACGTGCCGAA  AGCGGAAGAG  GCGCATTACG  CCTGGGGCTA  TCGTGACGGT
1351 AAAGCGGTGC  GCGTTTCGCC  GGGTATGCTG  GATGCACAAG  CCTATGGCGT
1401 GAAAACCAAC  GTGCAGGATA  TGGCGAACTG  GGTCATGGCA  AACATGGCGC
1451 CGGAGAACGT  TGCTGATGCC  TCACTTAAGC  AGGGCATCGC  GCTGGCGCAG
1501 TCGCGCTACT  GGCGTATCGG  GTCAATGTAT  CAGGGTCTGG  GCTGGGAGAT
1551 GCTCAACTGG  CCCGTGGAGG  CCAACACGGT  GGTCGAGACG  AGTTTTGGTA
1601 ATGTAGCACT  GGCGCCGTTG  CCCGTGGCAG  AAGTGAATCC  ACCGGCTCCC
1651 CCGGTCAAAG  CGTCCTGGGT  CCATAAAACG  GGCTCTACTG  GCGGGTTTTG
1701 CAGCTACGTG  GCCTTTATTC  CTGAAAAGCA  GATCGGTATT  GTGATGCTCG
1751 CGAATAACA  CTATCCGAAC  CCGGCACGCG  TTGAGGCGGC  ATACCATATC
1801 CTCGAGGCGC  TACAG
```

Fig. 15G. Nucleotide sequence of CAB1.4 gene

1	QVQLQQSGAE	LVKSGGSVKL	SCTASGFNIK	DSYMHVVRQG	PEQGLEWIGW
51	IDPENGDTFY	APKFQ GKATF	TTDTSSNTAY	LQLSSLTSED	TAVYYCNEGT
101	PTGPYYFDYW	GQGTTVTVSS	GGGSGGGGS	GGGSENVLT	QSPAIVSASP
151	GEKVTITCSA	SSSVSYMHWF	QOKPGTSPKL	VIYDTSNLAS	GVPARFSGSG
201	SGTSYSLTIS	RMEAEDAATY	YCQORDSYPL	TFGAGTKLEL	KRAATPVSEK
251	QLAEVVANTI	TPLMKAQSVF	GMAVAVIYQG	KPHYITFGKA	DIAANKPVTP
301	QTLFELGSIS	KTFTGVLGGD	AIARGEISLD	DAVTRYWPQL	TGKQWQGIRM
351	LDLATYTAGG	LPLQVPDEVT	DNASLLRFYQ	NWQPQWKPGT	TRLYANASIG
401	LFGALAVKPS	GMPYEQAMTT	RVLKPLKLDH	TWINVPKAEF	AHYAWGYRDG
451	KAVRVSPGML	DAQAYGVKTN	VQDMANWVMA	NMAPENVADA	SLKQGIALAQ
501	SRYWRIGSMY	QGLGWEMLNW	PVEANTVVET	SFGNVALAPL	PVAEVPNPAP
551	PVKASWVHKT	GSTGGFGSYV	AFIPEKQIGI	VMLANTSYPN	PARVEAAYHI
601	LEALQ				

Fig. 15H Amino acid sequence of CAB1.4 protein

H1CDR (154) GGCTTCAACATTAAAGACTCCTATATGCAC(183)
H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCCAG(273)
H3CDR (373) GGGCTCCCGACTGGGCCGTACTACTTTGACTAC(405)
L1CDR (553) AGTGCCAGCTCAAGTSTAAGTTACATGCAC(582)
L2CDR (628) GATACATCCAACCTGGCTTCT(648)
L3CDR (745) CAGCAAAGAGATAGTTACCCACTCAG(771)

Fig. 15I Nucleotide sequences of CAB1.6 CDRs

```
1 CAGGTGCAGC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGCTC
51 AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
101 TGCAGTGGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCCGAAGT TCCAGGGCAA
201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGGCTC
301 CCGACTGGGC CGTACTACTT TGACTIONTGG GGCCAAGGGA CCACGGTCAC
351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GCGGGTGGCG
401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCGTGTC TGCATCTCCA
451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAAGTG TAAGTTACAT
501 GCACTGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAACCTC GTGATTTATG
551 ATACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651 TGCCACTTAT TACTGCCAGC AAAGAGATAG TTACCCACTC ACGTTCGGTG
701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751 CAGCTGGCGG AGGTGGTTCG GAATACGATT ACCCCGCTGA TGAAAGCCCA
801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCTT
901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTTATCAA AACTGGCAGC
1151 CGCAGTGGAA GCCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGTGATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GGCGTATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTGAGACG AGTTTTGGTA
1601 ATGTAGCACT GGCGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CAGCTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG
```

Fig. 15J Nucleotide sequence of CAB1.6 gene

1	CAGGTGCAGC	TGCAGCAGTC	TGGGGCAGAA	CTTGTGAAAT	CAGGGGGCTC
51	AGTCAAGTTG	TCCTGCACAG	CTTCTGGCTT	CAACATTAAA	GACTCCTATA
101	TGCACTGGGT	GAGGCAGGGG	CCTGAACAGG	GCCTGGAGTG	GATTGGATGG
151	ATTGATCCTG	AGAATGGTGA	TACTGAATAT	GCCCCGAAGT	TCCAGGGCAA
201	GGCCACTTTT	ACTACAGACA	CATCCTCCAA	CACAGCCTAC	CTGCAGCTCA
251	GCAGCCTGAC	ATCTGAGGAC	ACTGCCGTCT	ATTATTGTAA	TGAGGGGCTC
301	CCGACTGGGC	CGTACTACTT	TGACTACTGG	GGCCAAGGGA	CCACGGTCAC
351	CGTCTCCTCA	GGTGGAGGCG	GTTCAGGCGG	AGGTGGCTCT	GGCGGTGGCG
401	GATCAGAAAA	TGTGCTCACC	CAGTCTCCAG	CAATCGTGTC	TGCATCTCCA
451	GGGGAGAAGG	TCACCATAAC	CTGCAGTGCC	AGCTCAAGTG	TAAGTTACAT
501	GCACTGGTTC	CAGCAGAAGC	CAGGCACTTC	TCCCAAACCTC	GTGATTTATG
551	ATACATCCAA	CCTGGCTTCT	GGAGTCCCTG	CTCGCTTCAG	TGGCAGTGGA
601	TCTGGGACCT	CTTACTCTCT	CACAATCAGC	CGAATGGAGG	CTGAAGATGC
651	TGCCACTTAT	TACTGCCAGC	AAAGAGATAG	TTACCCACTC	ACGTTCCGGTG
701	CTGGCACCAA	GCTGGAGCTG	AAACGGGCGG	CCACACCGGT	GTCAGAAAAA
751	CAGCTGGCGG	AGGTGGTCGC	GAATACGATT	ACCCCGCTGA	TGGCGGCCCA
801	GTCTGTTCCA	GGCATGGCGG	TGGCCGTTAT	TTATCAGGGA	AAACCGCACT
851	ATTACACATT	TGGCAAGGCC	GATATCGCGG	CGAATAAACC	CGTTACGCCT
901	CAGACCCTGT	TCGAGCTGGG	TTCTATAAGT	AAAACCTTCA	CCGGCGTTTT
951	AGGTGGGGAT	GCCATTGCTC	GCGGTGAAAT	TTCGCTGGAC	GATGCGGTGA
1001	CCAGATACTG	GCCACAGCTG	ACGGGCAAGC	AGTGGCAGGG	TATTCGTATG
1051	CTGGATCTCG	CCACCTACAC	CGCTGGCGGC	CTGCCGCTAC	AGGTACCGGA
1101	TGAGGTCACG	GATAACGCCT	CCCTGCTGCG	CTTTTATCAA	AACCTGGCAGC
1151	CGCAGTGGAA	GCCTGGCACA	ACGCGTCTTT	ACGCCAACGC	CAGCATCGGT
1201	CTTTTGGTG	CGCTGGCGGT	CAAACCTTCT	GGCATGCCCT	ATGAGCAGGC
1251	CATGACGACG	CGGGTCCTTA	AGCCGCTCAA	GCTGGACCAT	ACCTGGATTA
1301	ACGTGCCGAA	AGCGGAAGAG	GCGCATTACG	CCTGGGGCTA	TCGTGACGGT
1351	AAAGCGGTGC	GEGTTTCGCC	GGGTATGCTG	GATGCACAAG	CCTATGGCGT
1401	GAAAACCAAC	GTGCAGGATA	TGGCGAACTG	GGTCATGGCA	AACATGGCGC
1451	CGGAGAACGT	TGCTGATGCC	TCACTTAAGC	AGGGCATCGC	GCTGGCGCAG
1501	TCCGCTACT	GGCGTATCGG	GTCAATGTAT	CAGGGTCTGG	GCTGGGAGAT
1551	GCTCAACTGG	CCCGTGGAGG	CCAACACGGT	GGTCGAGACG	AGTTTTGGTA
1601	ATGTAGCACT	GGCGCCGTTG	CCCGTGGCAG	AAGTGAATCC	ACCGGCTCCC
1651	CCGGTCAAAG	CGTCCTGGGT	CCATAAAACG	GGCTCTACTG	GCGGGTTTGG
1701	CGCGTACGTG	GCCTTTATTC	CTGAAAAGCA	GATCGGTATT	GTGATGCTCG
1751	CGAATACAAG	CTATCCGAAC	CCGGCACGCG	TTGAGGCGGC	ATACCATATC
1801	CTCGAGGCGC	TACAG			

Fig. 15K Nucleotide sequence of CAB1.6i gene

H1CDR (154) GGCTTCAACATTAAAGACTCCTATATGCAC(183)
H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCAG(273)
H3CDR (373) GGGCTCCCGCTCGGGGCCATTTACAACGACTAC(405)
L1CDR (553) AGTGCCAGCTCAGCTGTATATGCCATGCAC(582)
L2CDR (628) GATACATCCAACCTGGCTTCT(648)
L3CDR (745) CAGCAAAGAGATAGTTACCCACTCACG(771)

Fig. 15L Nucleotide sequences of CAB1.7 CDRs

```
1  CAGGTGCAGC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGCTC
51 AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
101 TGCAGTGGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCGAAGT TCCAGGGCAA
201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGGCTC
301 CCGCTCGGGG CCATTTACAA CGACTACTGG GGCCAAGGGA CCACGGTCAC
351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GCGGTGGCG
401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCGTGTC TGCATCTCCA
451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAGCTG TATATGCCAT
501 GCACTGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAATC GTGATTTATG
551 ATACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651 TGCCACTTAT TACTGCCAGC AAAGAGATAG TTACCCACTC ACGTTCGGTG
701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751 CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCCGCTGA TGAAAGCCCA
801 GTCTGTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851 ATTACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTTATCAA AACTGGCAGC
1151 CGCAGTGGA GCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGTCAATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GGCGTATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTGAGACG AGTTTTGGTA
1601 ATGTAGCACT GCGCGCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CAGCTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG
```

Fig. 15M Nucleotide sequence of CAB1.7 gene

```
1  CAGGTGCAGC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGCTC
51 AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
101 TGCAGTGGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCCGAAGT TCCAGGGCAA
201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGGCTC
301 CCGCTCGGGG CCATTTACAA CGACTACTGG GGCCAAGGGA CCACGGTCAC
351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GGCGGTGGCG
401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCGTGTC TGCATCTCCA
451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAGCTG TATATGCCAT
501 GCACTGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAATC GTGATTTATG
551 ATACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651 TGCCACTTAT TACTGCCAGC AAAGAGATAG TTACCCACTC ACGTTCGGTG
701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751 CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCCGCTGA TGGCGGCCCA
801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTAECGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTATCAA AACTGGCAGC
1151 CGCAGTGGA GCCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGTCATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GCGTATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTGAGACG AGTTTTGGTA
1601 ATGTAGCACT GGCGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CGCGTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG
```

Fig. 15N Nucleotide sequence of CAB1.7i gene

H1CDR (154) GGCTTCAACATTAAAGACTCCTATATGCAC(183)
H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCCAG (273)
H3CDR (373) GGGACTCCGACTGGGCCGTACTACTTTGACTAC(405)
L1CDR (553) AGTGCCAGCTCAAGTGTAAGTTACATGCAC(582)
L2CDR (628) AGCACATCCAACCTGGCTTCT(648)
L3CDR (745) CAGCAAAGATCTAGTTACCCACTCACG(771)

Fig. 150 Nucleotide sequences of CAB1 CDRs

```
1  CAGGTGAAAC TGCAGCAGTC TGGGGCAGAA CTTGTGAGGT CAGGGACCCTC
51 AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAA A GACTCCTATA
101 TGCAC TGGTT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCCGAAGT TCCAGGGCAA
201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGACT
301 CCGACTGGGC CGTACTACTT TGACTACTGG GGCCAAGGGA CCACGGTCAC
351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GGCGGTGGCG
401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCATGTC TGCATCTCCA
451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAAGTG TAAGTTACAT
501 GCAC TGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAAC TC TGGATTTATA
551 GCACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651 TGCCACTTAT TACTGCCAGC AAAGATCTAG TTACCCACTC ACGTTCGGTG
701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751 CAGCTGGCGG AGGTGGTTCG GAATACGATT ACCCCGCTGA TGAAAGCCCA
801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTATCAA AACTGGCAGC
1151 CGCAGTGGA GCCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGT CATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GGCGTATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTGAGACG AGTTTTGGTA
1601 ATGTAGCACT GGCGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CAGCTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG
```

Fig. 15P Nucleotide sequence of CAB1 gene

H1CDR

(26) GFNIKDSYMH (35)

H2CDR (50) WIDPENGDTHEYAPKFQ (65)

H3CDR (99) GLPLGAIYNDY (109)

L1CDR (159) SASSSVSYMH (168)

L2CDR (184) DTSNLAS (190)

L3CDR (223) QQRDSYPLT (231)

Fig. 15Q Amino acid sequences of SW149.5 CDRs

H1CDR (154) GGCTTCAACATTAAAGACTCCTATATGCAC (183)
H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCCAG (273)
H3CDR (373) GGGCTCCCGCTCGGGGCCATTACAACTACTAC (405)
L1CDR (553) AGTGCCAGCTCAAGTGTAAAGTTACATGCAC (582)
L2CDR (628) GATACATCCAACCTGGCTTCT (648)
L3CDR (745) CAGCAAAGAGATAGTTACCCACTCACG (771)

Fig. 15R Nucleotide sequences of SW149.5 CDRs

```
1  CAGGTGCAGC  TGCAGCAGTC  TGGGGCAGAA  CTTGTGAAAT  CAGGGGGCTC
51  AGTCAAGTTG  TCCTGCACAG  CTTCTGGCTT  CAACATTAAA  GACTCCTATA
101 TGCCTGGGGT  GAGGCAGGGG  CCTGAACAGG  GCCTGGAGTG  GATTGGATGG
151 ATTGATCCTG  AGAATGGTGA  TACTGAATAT  GCCCCGAAGT  TCCAGGGCAA
201 GGCCACTTTT  ACTACAGACA  CATCCTCCAA  CACAGCCTAC  CTGCAGCTCA
251 GCAGCCTGAC  ATCTGAGGAC  ACTGCCGTCT  ATTATTGTAA  TGAGGGGCTC
301 CCGCTCGGGG  CCATTTACAA  CGACTACTGG  GGCCAAGGGA  CCACGGTCAC
351 CGTCTCCTCA  GGTGGAGGCG  GTTCAGGCGG  AGGTGGCTCT  GGCGGTGGCG
401 GATCAGAAAA  TGTGCTCACC  CAGTCTCCAG  CAATCGTGTC  TGCATCTCCA
451 GGGGAGAAGG  TCACCATAAC  CTGCAGTGCC  AGCTCAAGTG  TAAGTTACAT
501 GCACTGGTTC  CAGCAGAAGC  CAGGCACTTC  TCCCAAATC  GTGATTTATG
551 ATACATCCAA  CCTGGCTTCT  GGAGTCCCTG  CTCGCTTCAG  TGGCAGTGGA
601 TCTGGGACCT  CTTACTCTCT  CACAATCAGC  CGAATGGAGG  CTGAAGATGC
651 TGCCACTTAT  TACTGCCAGC  AAAGAGATAG  TTACCCACTC  ACGTTCGGTG
701 CTGGCACCAA  GCTGGAGCTG  AAACGGGCGG  CCACACCGGT  GTCAGAAAAA
751 CAGCTGGCGG  AGGTGGTCGC  GAATACGATT  ACCCCGCTGA  TGAAAGCCCA
801 GTCTGTTCCA  GGCATGGCGG  TGGCCGTTAT  TTATCAGGGA  AAACCGCACT
851 ATTACACATT  TGGCAAGGCC  GATATCGCGG  CGAATAAACC  CGTTACGCCT
901 CAGACCCTGT  TCGAGCTGGG  TTCTATAAGT  AAAACCTTCA  CCGGCGTTTT
951 AGGTGGGGAT  GCCATTGCTC  GCGGTGAAAT  TTCGCTGGAC  GATGCGGTGA
1001 CCAGATACTG  GCCACAGCTG  ACGGGCAAGC  AGTGGCAGGG  TATTCGTATG
1051 CTGGATCTCG  CCACCTACAC  CGCTGGCGGC  CTGCCGCTAC  AGGTACCGGA
1101 TGAGGTCACG  GATAACGCCT  CCCTGCTGCG  CTTTTATCAA  AACTGGCAGC
1151 CGCAGTGGAA  GCCTGGCACA  ACGCGTCTTT  ACGCCAACGC  CAGCATCGGT
1201 CTTTTTGGTG  CGCTGGCGGT  CAAACCTTCT  GGCATGCCCT  ATGAGCAGGC
1251 CATGACGACG  CGGGTCCTTA  AGCCGCTCAA  GCTGGACCAT  ACCTGGATTA
1301 ACGTGCCGAA  AGCGGAAGAG  GCGCATTACG  CCTGGGGCTA  TCGTGACGGT
1351 AAAGCGGTGC  GCGTTTCGCC  GGGTATGCTG  GATGCACAAG  CCTATGGCGT
1401 GAAAACCAAC  GTGCAGGATA  TGGCGAACTG  GGTCATGGCA  AACATGGCGC
1451 CGGAGAACGT  TGCTGATGCC  TCACTTAAGC  AGGGCATCGC  GCTGGCGCAG
1501 TCGCGCTACT  GGCGTATCGG  GTCAATGTAT  CAGGGTCTGG  GCTGGGAGAT
1551 GCTCAACTGG  CCCGTGGAGG  CCAACACGGT  GGTCGAGACG  AGTTTTGGTA
1601 ATGTAGCACT  GGCGCCGTTG  CCCGTGGCAG  AAGTGAATCC  ACCGGCTCCC
1651 CCGGTCAAAG  CGTCCTGGGT  CCATAAAACG  GGCTCTACTG  GCGGGTTTGG
1701 CAGCTACGTG  GCCTTTATTC  CTGAAAAGCA  GATCGGTATT  GTGATGCTCG
1751 CGAATACAAG  CTATCCGAAC  CCGGCACGCG  TTGAGGCGGC  ATACCATATC
1801 CTCGAGGCGC  TACAG
```

Fig. 15S Nucleotide sequence of SW149.5 gene

```
1  ACACCGGTGT CAGAAAAACA GCTGGCGGAG GTGGTCGCGA ATACGATTAC
51  CCCGCTGATG AAAGCCCAGT CTGTTCCAGG CATGGCGGTG GCCGTTATTT
101 ATCAGGGAAA ACCGCACTAT TACACATTG GCAAGGCCGA TATCGCGGCG
151 AATAAACCCG TTACGCCTCA GACCCTGTTC GAGCTGGGTT CTATAAGTAA
201 AACCTTCACC GGC GTTTTAG GTGGGGATGC CATTGCTCGC GGTGAAATTT
251 CGCTGGACGA TGC GGTGACC AGATACTGGC CACAGCTGAC GGGCAAGCAG
301 TGGCAGGGTA TTCGTATGCT GGATCTCGCC ACCTACACCG CTGGCGGCCT
351 GCCGCTACAG GTACCGGATG AGGTCACGGA TAACGCCTCC CTGCTGCGCT
401 TTTATCAAAA CTGGCAGCCG CAGTGGAAGC CTGGCACAAC GCGTCTTTAC
451 GCCAACGCCA GCATCGGTCT TTTTGGTGCG CTGGCGGTCA AACCTTCTGG
501 CATGCCCTAT GAGCAGGCCA TGACGACGCG GGTCCTTAAG CCGCTCAAGC
551 TGGACCATAC CTGGATTAAC GTGCCGAAAG CGGAAGAGGC GCATTACGCC
601 TGGGGCTATC GTGACGGTAA AGCGGTGCGC GTTTCGCCGG GTATGCTGGA
651 TGCACAAGCC TATGGCGTGA AAACCAACGT GCAGGATATG GCGAACTGGG
701 TCATGGCAAA CATGGCGCCG GAGAACGTTG CTGATGCCTC ACTTAAGCAG
751 GGCATCGCGC TGGCGCAGTC GCGCTACTGG CGTATCGGGT CAATGTATCA
801 GGGTCTGGGC TGGGAGATGC TCAACTGGCC CGTGGAGGCC AACACGGTGG
851 TCGAGACGAG TTTTGGTAAT GTAGCACTGG CGCCGTTGCC CGTGGCAGAA
901 GTGAATCCAC CGGCTCCCCC GGTCAAAGCG TCCTGGGTCC ATAAAAACGGG
951 CTCTACTGGC GGGTTTGGCA GCTACGTGGC CTTTATTCTT GAAAAGCAGA
1001 TCGGTATTGT GATGCTCGCG AATAACAAGCT ATCCGAACCC GGCACGCGTT
1051 GAGGCGGCAT ACCATATCCT CGAGGCGCTA CAG
```

Fig. 15T Nucleotide sequence of BLA gene


```
1  CAGGTGAAAC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGCTC
51  AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
101 TGCAC TGGTT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCCGAAGT TCCAGGGCAA
201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGACT
301 CCGACTGGGC CGTACTACTT TGACTACTGG GGCCAAGGGA CCACGGTCAC
351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GCGGGTGGCG
401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCATGTC TGCATCTCCA
451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAAGTG TAAGTTACAT
501 GCACTGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAAC TC GTGATTTATA
551 GCACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651 TGCCACTTAT TACTGCCAGC AAAGATCTAG TTACCCACTC ACGTTCGGTG
701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751 CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCCGCTGA TGAAAGCCCA
801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTACAG GATAACGCCT CCCTGCTGCG CTTTTATCAA AACTGGCAGC
1151 CGCAGTGGA GCCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGTCATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GCGGTATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTCGAGACG AGTTTTGGTA
1601 ATGTAGCACT GCGGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CAGCTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG
```

Fig. 15U Nucleotide sequence of CAB1.1 gene

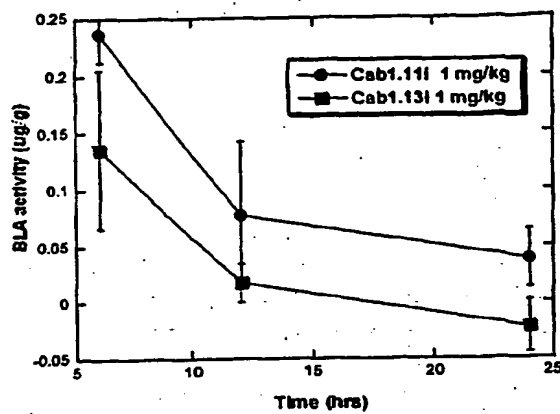


Figure 16

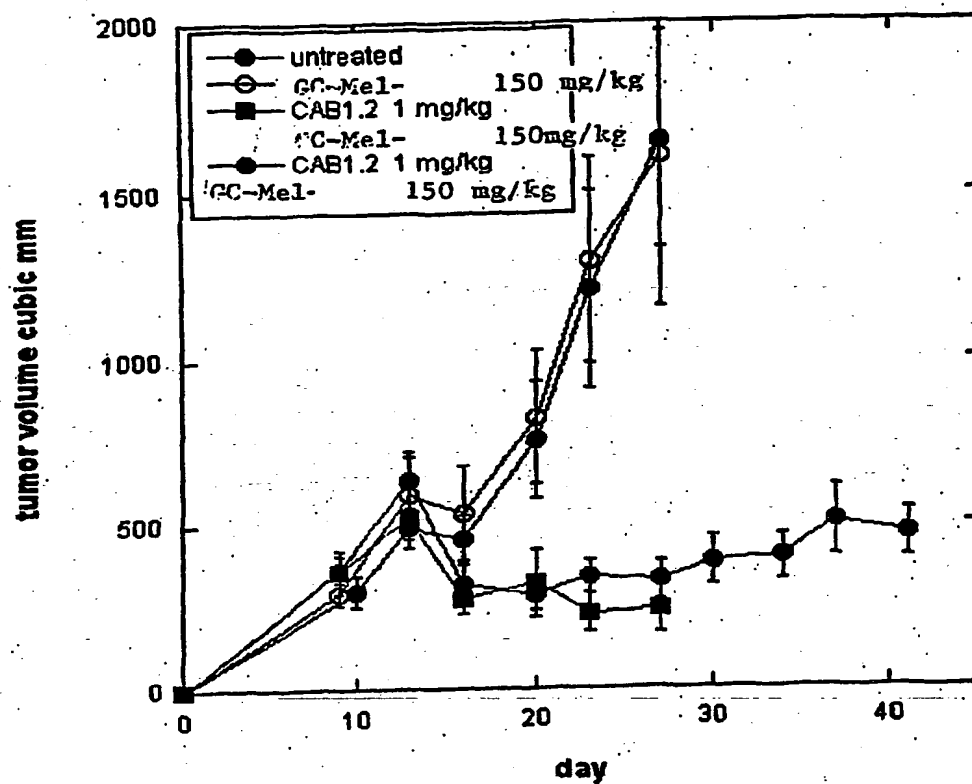


Figure 17

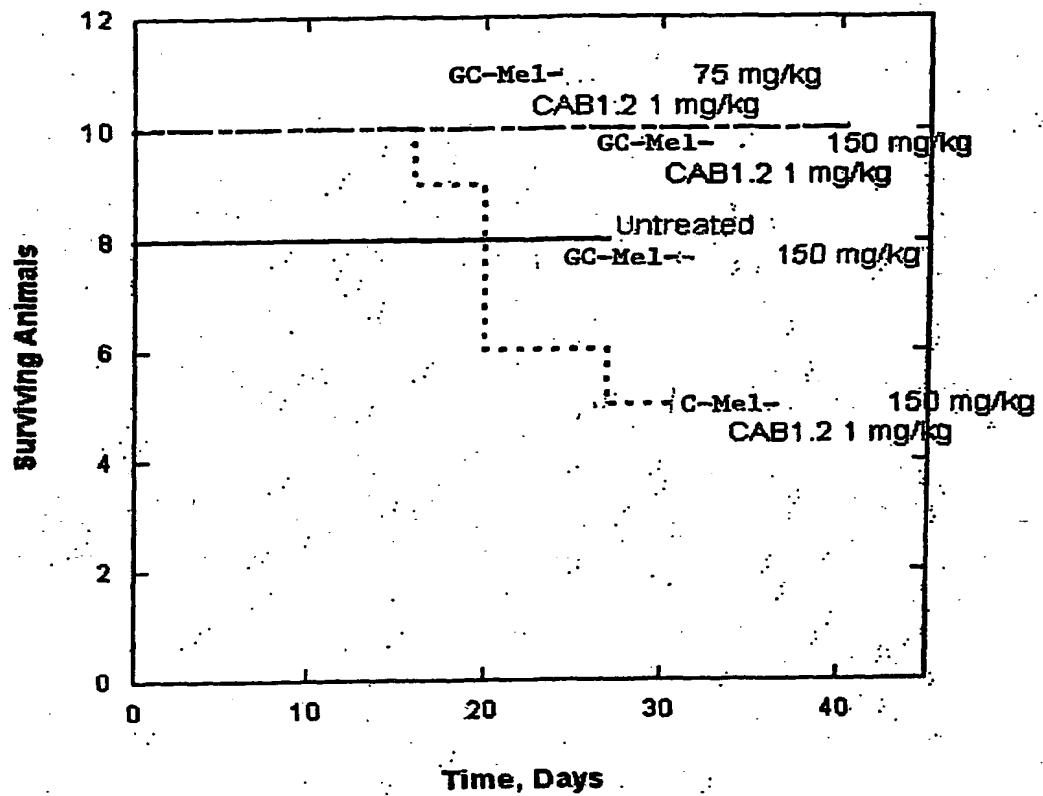


Figure 18

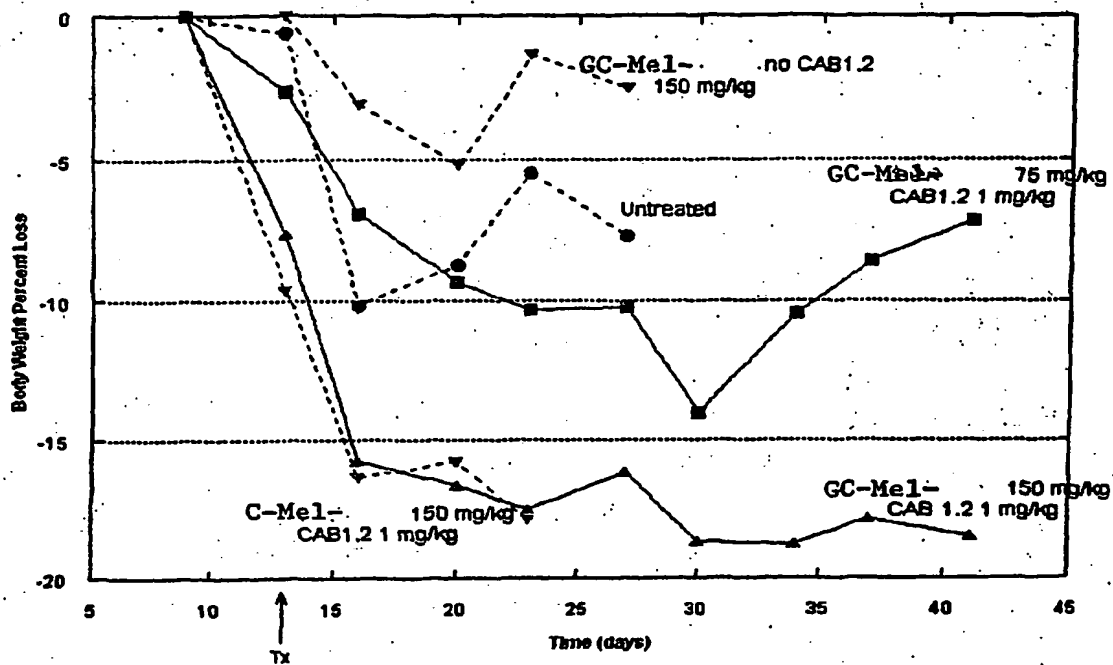


Figure 19

Animal weight effects

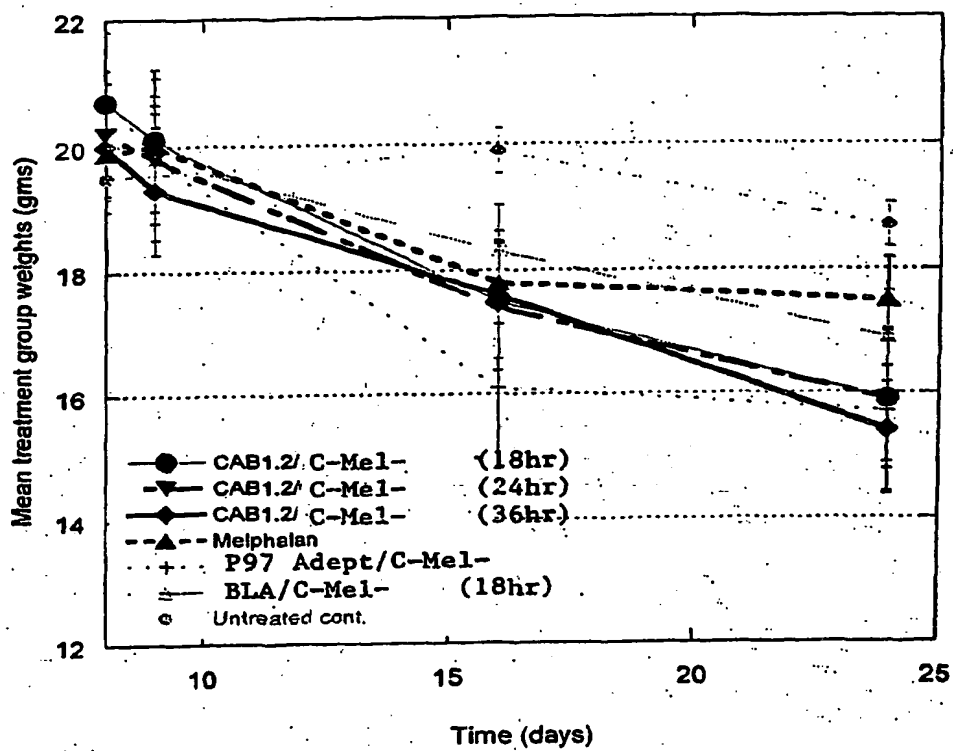


Figure 20

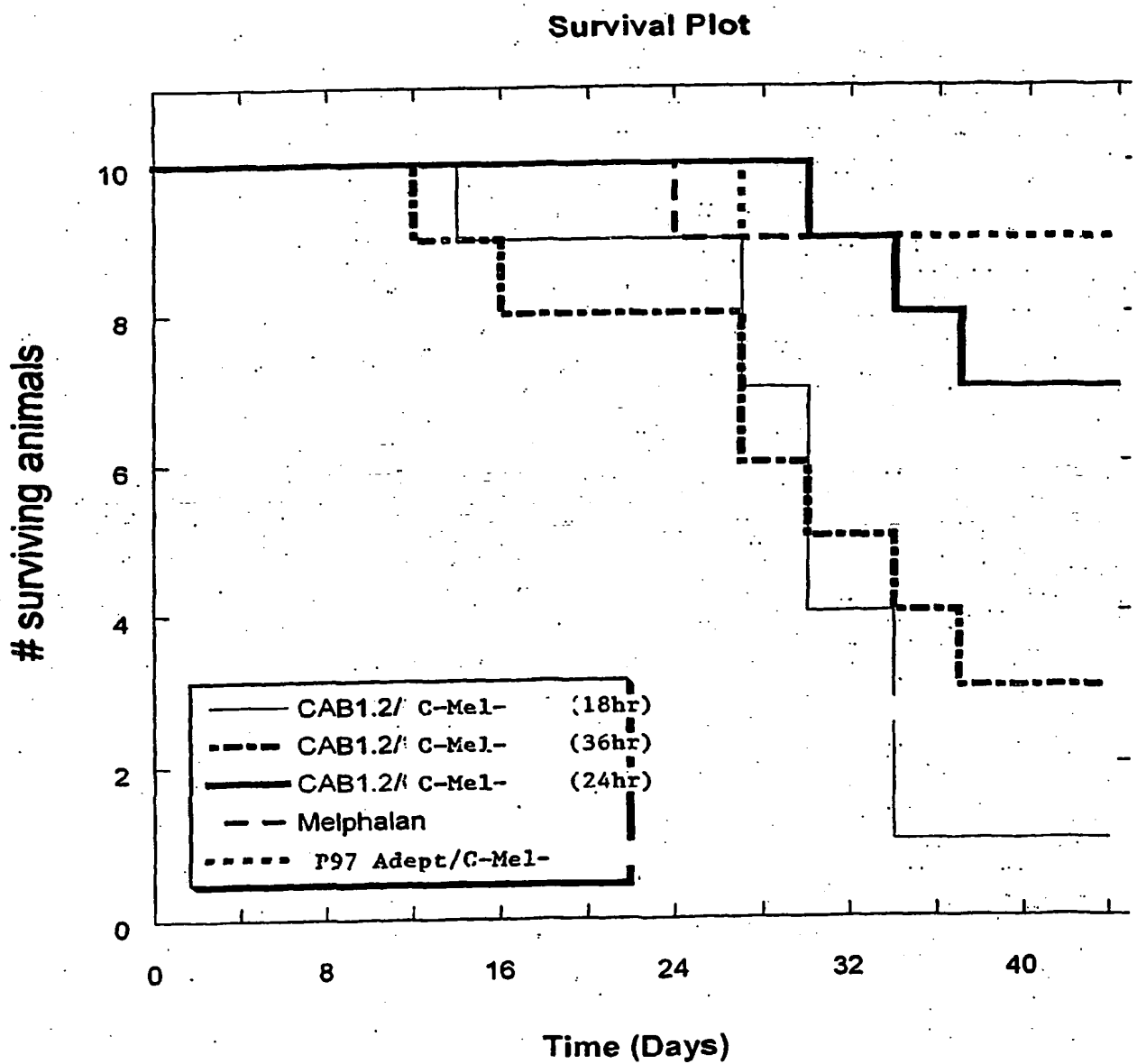
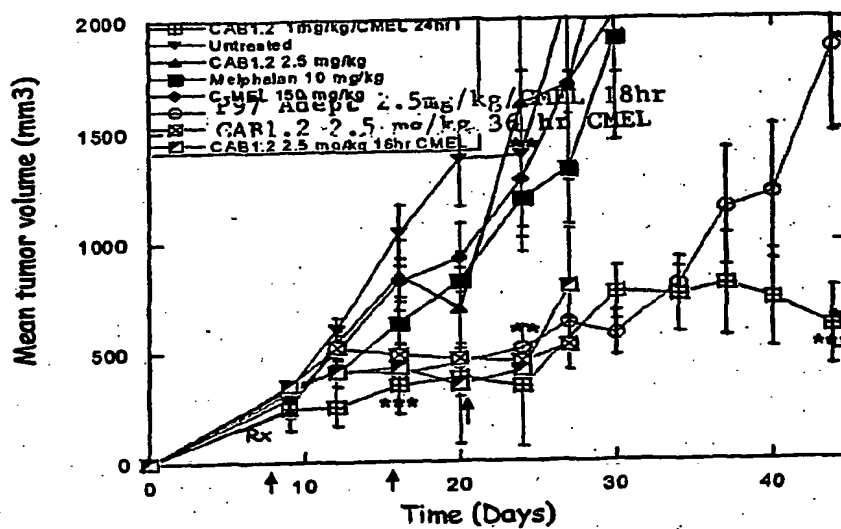


Figure 21

CAB1 Proof of Principle – Efficacy#



* $p < 0.05$ sgn17 vs CAB1.2(24h)

** $p < 0.05$ untreated vs CAB1.2(18,24,36h)

***GC observed in 2 animals: 1 Day 16; 1 Day 44

Figure 22

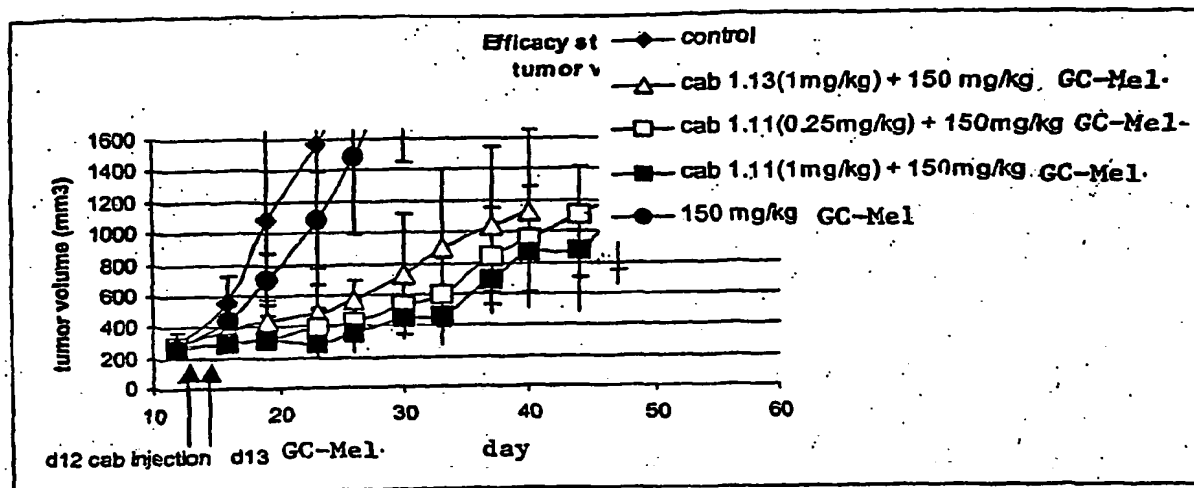


Figure 23

1	QVQLQQSGAE	LVKSGGSVKL	SCTASGFNIK	DSYMHWVRQG	PEQGLEWIGW
51	IDPENGDTY	APKFQGKATF	TTDTSSNTAY	LQLSSLTSED	TAVYYCNEGT
101	PTGPYYFDYW	GQGTTVTVSS	GGGSGGGGS	GGGSENVLT	QSPAIVSASP
151	GEKVTITCSA	SSSVSYMHWF	QKPGTSPKL	VIYSTSNLAS	GVPARFSGSG
201	SGTSYSLTIS	RMEAEDAATY	YCQQRSSYPL	TFGAGTKLEL	KRAATPVSEK
251	QLAEVVANTI	TPLMAAQSV	GMAVAVIYQG	KPHYITFGKA	DIAANKPVTP
301	QTLFELGSIS	KTFTGVLGGD	AIARGEISLD	DAVTRYWPQL	TGKQWQGIRM
351	LDLATYTAGG	LPLQVPDEVT	DNASLLRFYQ	NWQPQWKPGT	TRLYANASIG
401	LFGALAVKPS	GMPYEQAMTT	RVLKPLKLDH	TWINVPKAE	AHYAWGYRDG
451	KAVRVSPGML	DAQAYGVKTN	VQDMANWVMA	NMAPENVADA	SLKQGIALLQ
501	SRYWRIGSMY	QGLGWEMLNW	PVEANTVET	SFGNVALAPL	PVAEVNPPAP
551	PVKASWVHKT	GSTGGFGAYV	AFIPEKQIGI	VMLANTSYPN	PARVEAAYHI
601	LEALQ				

Figure 24A

1	CAGGTGCAGC	TGCAGCAGTC	TGGGGCAGAA	CTTGTGAAAT	CAGGGGGCTC
51	AGTCAAGTTG	TCCTGCACAG	CTTCTGGCTT	CAACATTAAA	GACTCCTATA
101	TGCACTGGGT	GAGGCAGGGG	CCTGAACAGG	GCCTGGAGTG	GATTGGATGG
151	ATTGATCCTG	AGAATGGTGA	TACTGAATAT	GCCCCGAAGT	TCCAGGGCAA
201	GGCCACTTTT	ACTACAGACA	CATCCTCCAA	CACAGCCTAC	CTGCAGCTCA
251	GCAGCCTGAC	ATCTGAGGAC	ACTGCCGTCT	ATTATTGTAA	TGAGGGGACT
301	CCGACTGGGC	CGTACTACTT	TGACTACTGG	GGCCAAGGGA	CCACGGTCAC
351	CGTCTCCTCA	GGTGGAGGCG	G TTCAGGCGG	AGGTGGCTCT	GGCGGTGGCG
401	GATCAGAAAA	TGTGCTCACC	CAGTCTCCAG	CAATCGTGTC	TGCATCTCCA
451	GGGGAGAAGG	TCACCATAAC	CTGCAGTGCC	AGCTCAAGTG	TAAGTTACAT
501	GCACTGGTTC	CAGCAGAAGC	CAGGCACTTC	TCCCAAACCT	GTGATTTATA
551	GCACATCCAA	CCTGGCTTCT	GGAGTCCCTG	CTCGCTTCAG	TGGATTGGA
601	TCTGGGACCT	CTTACTCTCT	CACAATCAGC	CGAATGGAGG	CTGAAGATGC
651	TGCCACTTAT	TACTGCCAGC	AAAGATCTAG	TTACCCACTC	ACGTTTCGGTG
701	CTGGCACCAA	GCTGGAGCTG	AAACGGGCGG	CCACACCGGT	GTCAGAAAAA
751	CAGCTGGCGG	AGGTGGTCGC	GAATACGATT	ACCCCGCTGA	TGGCGGCCCA
801	GTCTGTTCCA	GGCATGGCGG	TGGCCGTTAT	TTATCAGGGA	AAACCGCACT
851	ATTACACATT	TGGCAAGGCC	GATATCGCGG	CGAATAAACC	CGTTACGCCT
901	CAGACCCTGT	TCGAGCTGGG	TCTATAAGT	AAAACCTTCA	CCGGCGTTTT
951	AGGTGGGGAT	GCCATTGCTC	GCGGTGAAAT	TTCGCTGGAC	GATGCGGTGA
1001	CCAGATACTG	GCCACAGCTG	ACGGGCAAGC	AGTGGCAGGG	TATTCGTATG
1051	CTGGATCTCG	CCACCTACAC	CGCTGGCGGC	CTGCCGCTAC	AGGTACCGGA
1101	TGAGGTCACG	GATAACGCCT	CCCTGCTGCG	CTTTTATCAA	AACTGGCAGC
1151	CGCAGTGGAA	GCCTGGCACA	ACGCGTCTTT	ACGCCAACGC	CAGCATCGGT
1201	CTTTTTGGTG	CGCTGGCGGT	CAAACCTTCT	GGCATGCCCT	ATGAGCAGGC
1251	CATGACGACG	CGGGTCCTTA	AGCCGCTCAA	GCTGGACCAT	ACCTGGATTA
1301	ACGTGCCGAA	AGCGGAAGAG	GCGCATTACG	CCTGGGGGCTA	TCGTGACGGT
1351	AAAGCGGTGC	GCGTTTCGCC	GGGTATGCTG	GATGCACAAG	CCTATGGCGT
1401	GAAAACCAAC	GTGCAGGATA	TGGCGAACTG	GGTCATGGCA	AACATGGCGC
1451	CGGAGAACGT	TGCTGATGCC	TCACTTAAGC	AGGGCATCGC	GCTGGCGCAG
1501	TCGCGCTACT	GGCGTATCGG	GTCAATGTAT	CAGGGTCTGG	GCTGGGAGAT
1551	GCTCAACTGG	CCCGTGGAGG	CCAACACGGT	GGTCGAGACG	AGTTTTGGTA
1601	ATGTAGCACT	GGCGCCGTTG	CCCGTGGCAG	AAGTGAATCC	ACCGGCTCCC
1651	CCGGTCAAAG	CGTCCTGGGT	CCATAAAACG	GGCTCTACTG	GCGGGTTTGG
1701	CGCGTACGTG	GCCTTTATTC	CTGAAAAGCA	GATCGGTATT	GTGATGCTCG
1751	CGAATAACAAG	CTATCCGAAC	CCGGCACGCG	TTGAGGCGGC	ATACCATATC
1801	CTCGAGGCGC	TACAG			

Figure 24B

1 QVQLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWVRQG PEQGLEWIGW
51 IDPENGDT EY APKFQ GKATF TTD TSSNTAY LQLSSLTSED TAVYYCNEGL
101 PLGAIYNDYW GQGT TVTVSS GGGGSGGGGS GGGGSENVLT QSPAIVSASP
151 GEKVTITCSA SSAVYAMHWF QOKPGTSPKL VIYSTSNLAS GVPARFSGSG
201 SGTSYSLTIS RMEAEDAATY YCQQRDSYPL TFGAGTKLEL KRAATPVSEK
251 QLAEVVANTI TPLMAAQSVPM GMAVAVIYQG KPHYTTFGKA DIAANKPVTP
301 QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351 LDLATYTAGG LPLQVPDEVT DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401 LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451 KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501 SRYWRIGSMY QGLGWEMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551 PVKASWVHKT GSTGGFGAYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601 LEALQ

Figure 24C

1	CAGGTGCAGC	TGCAGCAGTC	TGGGGCAGAA	CTTGTGAAAT	CAGGGGGCTC
51	AGTCAAGTTG	TCCTGCACAG	CTTCTGGCTT	CAACATTAAA	GACTCCTATA
101	TGCACTGGGT	GAGGCAGGGG	CCTGAACAGG	GCCTGGAGTG	GATTGGATGG
151	ATTGATCCTG	AGAATGGTGA	TACTGAATAT	GCCCCGAAGT	TCCAGGGCAA
201	GGCCACTTTT	ACTACAGACA	CATCCTCCAA	CACAGCCTAC	CTGCAGCTCA
251	GCAGCCTGAC	ATCTGAGGAC	ACTGCCGTCT	ATTATTGTAA	TGAGGGGCTC
301	CCGCTCGGGG	CCATTTACAA	CGACTACTGG	GGCCAAGGGA	CCACGGTCAC
351	CGTCTCCTCA	GGTGGAGGCG	GTTCAGGCGG	AGGTGGCTCT	GGCGGTGGCG
401	GATCAGAAAA	TGTGCTCACC	CAGTCTCCAG	CAATCGTGTC	TGCATCTCCA
451	GGGGAGAAGG	TCACCATAAC	CTGCAGTGCC	AGCTCAGCTG	TATATGCCAT
501	GCACTGGTTC	CAGCAGAAGC	CAGGCACTTC	TCCCAAACCTC	GTGATTTATA
551	GCACATCCAA	CCTGGCTTCT	GGAGTCCCTG	CTCGCTTCAG	TGGCAGTGGA
601	TCTGGGACCT	CTTACTCTCT	CACAATCAGC	CGAATGGAGG	CTGAAGATGC
651	TGCCACTTAT	TACTGCCAGC	AAAGAGATAG	TTACCCACTC	ACGTTTCGGTG
701	CTGGCACCAA	GCTGGAGCTG	AAACGGGCGG	CCACACCGGT	GTCAGAAAAA
751	CAGCTGGCGG	AGGTGGTCGC	GAATACGATT	ACCCCGCTGA	TGGCGGCCCA
801	GTCTGTTCCA	GGCATGGCGG	TGGCCGTTAT	TTATCAGGGA	AAACCGCACT
851	ATTACACATT	TGGCAAGGCC	GATATCGCGG	CGAATAAACC	CGTTACGCCT
901	CAGACCCTGT	TCGAGCTGGG	TTCTATAAGT	AAAACCTTCA	CCGGCGTTTT
951	GGTGGGGAT	GCCATTGCTC	GCGGTGAAAT	TTCGCTGGAC	GATGCGGTGA
1001	CCAGATACTG	GCCACAGCTG	ACGGGCAAGC	AGTGGCAGGG	TATTCGTATG
1051	CTGGATCTCG	CCACCTACAC	CGCTGGCGGC	CTGCCGCTAC	AGGTACCGGA
1101	TGAGGTCACG	GATAACGCCT	CCCTGCTGCG	CTTTTATCAA	AACTGGCAGC
1151	CGCAGTGGAA	GCCTGGCACA	ACGCGTCTTT	ACGCCAACGC	CAGCATCGGT
1201	CTTTTTTGGT	CGCTGGCGGT	CAAACCTTCT	GGCATGCCCT	ATGAGCAGGC
1251	CATGACGACG	CGGGTCCTTA	AGCCGCTCAA	GCTGGACCAT	ACCTGGATTA
1301	ACGTGCCGAA	AGCGGAAGAG	GCGCATTACG	CCTGGGGCTA	TCGTGACGGT
1351	AAAGCGGTGC	GCGTTTCGCC	GGGTATGCTG	GATGCACAAG	CCTATGGCGT
1401	GAAAACCAAC	GTGCAGGATA	TGGCGAACTG	GGTCATGGCA	AACATGGCGC
1451	CGGAGAACGT	TGCTGATGCC	TCACTTAAGC	AGGGCATCGC	GCTGGCGCAG
1501	TCGCGCTACT	GGCGTATCGG	GTCAATGTAT	CAGGGTCTGG	GCTGGGAGAT
1551	GCTCAACTGG	CCCGTGGAGG	CCAACACGGT	GGTCGAGACG	AGTTTTGGTA
1601	ATGTAGCACT	GGCGCCGTTG	CCCGTGGCAG	AAGTGAATCC	ACCGGCTCCC
1651	CCGGTCAAAG	CGTCCTGGGT	CCATAAAACG	GGCTCTACTG	GCGGGTTTGG
1701	CGCGTACGTG	GCCTTTATTC	CTGAAAAGCA	GATCGGTATT	GTGATGCTCG
1751	CGAATACAAG	CTATCCGAAC	CCGGCACGCG	TTGAGGCGGC	ATACCATATC
1801	CTCGAGGCGC	TACAG			

Figure 24 D

1 DIVLTQSPAS LSVSLGQRAT MSCRAGESVD IFGVGFLHWY QOKPGQPPKL
51 LIYRASNLGS GIPVRFSGTG SGTDFTLIID PVEADDEVATY YCQQTNEDPY
101 TFGGGTKLEI KGGGSGGGG SGGGSGGGG SGGGSGGGG SEVQLQQSGA
151 ELVEPGASVK LSCTASGFNI KDTYMHVVKQ RPEQGLEWIG RIDPANGNSK
201 YVPKFQ GKAT ITADTSSNTA YLQLTSLTSE DTAVYYCAPE GYYVSDYAMA
251 YWGQGTSTVTV SSTPVSEKQL AEVVANTITP LMAAQSVPGM AVAVIYQGKP
301 HYYTFGKADI AANKPVTPQT LFELGSISKT FTGVLGGDAI ARGEISLDDA
351 VTRYWPQLTG KQWQGIRMLD LATYTAGGLP LQVPDEVTDN ASLLRFYQNW
401 QPQWKPGTTR LYANASIGLF GALAVKPSGM PYEQAMTTRV LKPLKLDHTW
451 INVPKAEEAH YAWGYRDGKA VRVSPGMLDA QAYGVKTNVQ DMANWVMANM
501 APENVADASL KQGIALAQSR YWRIGSMYQG LGWEMLNWPV EANTVVETSF
551 GNVALAPLPV AEVNPPAPPV KASWVHKTGS TGGFGAYVAF IPEKQIGIVM
601 LANTSYPNPA RVEAAYHILE ALQ

Figure 25A

1	GACATCGTCC	TGACCCAGAG	CCCGGCAAGC	CTGTCTGTTT	CCCTGGGCCA
51	GCGTGCCACT	ATGTCCTGCA	GAGCGGGTGA	GTCTGTTGAC	ATTTTCGGTG
101	TCGGTTTTCT	GCACTGGTAC	CAACAGAAAC	CGGGTCAGCC	GCCAAACTG
151	CTGATCTATC	GTGCTTCTAA	CCTGGAGTCC	GGCATCCCGG	TACGTTTCTC
201	CGGTACTGGC	TCTGGTACTG	ATTTTACCCT	GATTATCGAC	CCGGTGGAAAG
251	CAGACGATGT	TGCCACCTAC	TATTGCCAGC	AGACCAACGA	GGATCCGTAC
301	ACCTTCGGTG	GCGGTACTAA	ACTGGAGATC	AAAGGCGGTG	GTGGTTCTGG
351	TGGTGGTGGT	AGCGGTGGCG	GTGGTAGCGG	TGGCGGTGGC	AGCGGTGGTG
401	GTGGCTCTGG	TGGCGGTGGC	TCTGAAGTGC	AGCTGCAGCA	GTCCGGTGGC
451	GAGCTCGTTG	AACCGGGCGC	TTCTGTGAAA	CTGTCTTGCA	CTGCATCTGG
501	TTTCAACATT	AAGGACACCT	ACATGCACTG	GGTGAACAA	CGCCCGGAAC
551	AGGGTCTGGA	GTGGATCGGT	CGCATCGATC	CGGCTAACGG	TAACAGCAAA
601	TACGTGCCAA	AATTCCAGGG	TAAAGCAACC	ATCACTGCTG	ATACCTCCTC
651	TAACACTGCT	TACCTGCAGC	TGACTTCCCT	GACTAGCGAA	GACACCGCGG
701	TTTATTACTG	CGCTCCGTTT	GGCTACTATG	TCAGCGATTA	CGCAATGGCC
751	TACTGGGGTC	AGGGCACCTC	TGTTACCGTT	TCTAGCACAC	CGGTGTCAGA
801	AAAACAGCTG	GCGGAGGTGG	TCGCGAATAC	GATTACCCCG	CTGATGGCGG
851	CCCAGTCTGT	TCCAGGCATG	GCGGTGGCCG	TTATTTATCA	GGGAAAACCG
901	CACTATTACA	CATTTGGCAA	GGCCGATATC	GCGGCGAATA	AACCCGTTAC
951	GCCTCAGACC	CTGTTGAGC	TGGGTTCTAT	AAGTAAAACC	TTCACCGGCG
1001	TTTTAGGTGG	GGATGCCATT	GCTCGCGGTG	AAATTTGCTG	GGACGATGCG
1051	GTGACCAGAT	ACTGGCCACA	GCTGACGGGC	AAGCAGTGGC	AGGGTATTCTG
1101	TATGCTGGAT	CTCGCCACCT	ACACCGCTGG	CGGCCTGCCG	CTACAGGTAC
1151	CGGATGAGGT	CACGGATAAC	GCCTCCCTGC	TGCGCTTTTA	TCAAAACTGG
1201	CAGCCGCACT	GGAAGCCTGG	CACAACGCGT	CTTTACGCCA	ACGCCAGCAT
1251	CGGTCTTTTT	GGTGCCTGG	CGGTCAAACC	TTCTGGCATG	CCCTATGAGC
1301	AGGCCATGAC	GACGCGGGTC	CTTAAGCCGC	TCAAGCTGGA	CCATACCTGG
1351	ATTAACGTGC	CGAAAGCGGA	AGAGGCGCAT	TACGCCTGGG	GCTATCGTGA
1401	CGGTAAAGCG	GTGCGCGTTT	CGCCGGGTAT	GCTGGATGCA	CAAGCCTATG
1451	GCGTGAAAAC	CAACGTGCAG	GATATGGCGA	ACTGGGTCAT	GGCAAACATG
1501	GCGCCGGAGA	ACGTTGCTGA	TGCCTCACTT	AAGCAGGGCA	TCGCGCTGGC
1551	GCAGTCGCGC	TACTGGCGTA	TCGGGTCAAT	GTATCAGGGT	CTGGGCTGGG
1601	AGATGCTCAA	CTGGCCCGTG	GAGGCCAACA	CGGTGGTTCG	GACGAGTTTT
1651	GGTAATGTAG	CACTGGCGCC	GTTGCCCGTG	GCAGAAGTGA	ATCCACCGGC
1701	TCCCCCGGTC	AAAGCGTCCT	GGGTCCATAA	AACGGGCTCT	ACTGGCGGGT
1751	TTGGCGCGTA	CGTGGCCTTT	ATTCCTGAAA	AGCAGATCGG	TATTGTGATG
1801	CTCGCGAATA	CAAGCTATCC	GAACCCGGCA	CGCGTTGAGG	CGGCATACCA
1851	TATCCTCGAG	GCGCTACAG			

Figure 25B

Case ID	ASM	Sample ID	Sample Pathology
<u>CI0000000255</u>	DF5	FR00005C7B	Adenocarcinoma of lung
<u>CI00000005496</u>	FF5	FR5B337147	Adenocarcinoma of lung
<u>CI0000011577</u>	FF1	FR5B34059F	Adenocarcinoma of lung
<u>CI70000000241</u>	AF4	FR00033A78	Adenocarcinoma of lung
<u>CI00000007518</u>	AF5	FR0001FD15	Carcinoma of lung, squamous cell
<u>CI00000008475</u>	HF4	FR65EE0784	Adenocarcinoma of colon, metastatic
<u>CI0000015252</u>	FF2	FR5B342166	Adenocarcinoma of colon

Figure 26

26_A	26_B	26_C	26_D	26_E
26_F	26_G	26_H	26_I	26_J

FIGURE 26

FIG. 26 - A

Case Diagnosis	Issue of Origin/Site of Finding	H/E	Anti-H
Adenocarcinoma of lung Grade: AJCC G3: Poorly differentiated Stage: IIIA	Lung/Lung	<u>4X</u> <u>20X</u>	Immunoger <u>4x</u>
Adenocarcinoma of lung Grade: AJCC G3: Poorly differentiated Stage: IIIB	Lung/Lung	<u>4X</u> <u>20X</u>	
Adenocarcinoma of lung Grade: AJCC G2: Moderately differentiated Stage: IIIA	Lung/Lung	<u>4X</u> <u>20X</u>	
Adenocarcinoma of lung Grade: AJCC G2: Moderately differentiated Stage: IIIA	Lung/Lung	<u>4X</u> <u>20X</u>	
Carcinoma of lung, squamous cell Grade: AJCC G3: Poorly differentiated Stage: IIIA	Lung/Lung	<u>4X</u> <u>20X</u>	
Adenocarcinoma of colon, metastatic Grade: Not Reported Stage: IV	Colon/Liver	<u>4X</u> <u>20X</u>	Immun Fibr No <u>4x</u>
Adenocarcinoma of colon Grade: AJCC G3: Poorly differentiated Stage: IIIB	Cecum/Cecum	<u>4X</u> <u>20X</u>	

FIG. 26-3

human Cytokeratin AE1/AE3	CAB/GCR3708 (0.2ug/ml)	CAB/GCR55
<p>Immunogenicity: Tumor(100%, Variable to 3+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 1 20x <u>SF00029758</u></p>	<p>Immunogenicity: Tumor(100%, Variable to 3+ Cyto) Mixed inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x 20x <u>SF00029756</u></p>	<p>Immunogenicity: Tumor(100%, Variable to 3+ Cyto) Mixed inflammatory cells(Variable to 1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x <u>SF000</u></p>
	<p>Immunogenicity: Tumor(15%, Variable to 3+ Cyto) Intra-alveolar macrophages(Variable to 2+ Cyto) Mixed inflammatory cells(Variable to 2+ Cyto) Specificity: High 4x 20x <u>SF0002975B</u></p>	<p>Immunogenicity: Tumor(15%, Variable to 3+ Cyto) Intra-alveolar macrophages(Variable to 2+ Cyto) Mixed inflammatory cells(Variable to 2+ Cyto) Specificity: High 4x <u>SF000</u></p>
	<p>Immunogenicity: Tumor(100%, 2+ Cyto) Cellular stroma(1+ Cyto) Chronic inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x 20x <u>SF0002977E</u></p>	<p>Immunogenicity: Tumor(100%, 2+ Cyto) Cellular stroma(1+ Cyto) Chronic inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x <u>SF000</u></p>
	<p>Immunogenicity: Tumor(75%, Variable to 3+ Cyto) Cellular Stroma(Variable to 2+ Cyto) Necrosis(Variable to 2+ EC) Intra-alveolar macrophages(Variable to 2+ Cyto) Specificity: High 4x 20x <u>SF0002978B</u></p>	<p>Immunogenicity: Tumor(75%, Variable to 3+ Cyto) Cellular Stroma(Variable to 2+ Cyto) Necrosis(Variable to 2+ EC) Intra-alveolar macrophages(Variable to 2+ Cyto) Specificity: High 4x <u>SF000</u></p>
	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Fibrotic stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x <u>SF0002975F</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Fibrotic stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x <u>SF000</u></p>
<p>Immunogenicity: Tumor(98%, Variable to 3+ Cyto) Mem. Variable to 3+ Cyto) Fibrotic stroma(Variable to 1+ Cyto) Normal liver parenchyma(2+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 20x <u>SF0002976A</u></p>	<p>Immunogenicity: Tumor(95%, Variable to 3+ Cyto) Mem. Variable to 3+ Cyto) Fibrotic stroma(Variable to 1+ Cyto) Normal liver parenchyma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x <u>SF00029768</u> Normal liver parenchyma shows positive staining (1+)</p>	<p>Immunogenicity: Tumor(95%, Variable to 3+ Cyto) Mem. Variable to 3+ Cyto) Fibrotic stroma(Variable to 1+ Cyto) Normal liver parenchyma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x <u>SF000</u></p>
	<p>Immunogenicity: Tumor(85%, Variable to 3+ Cyto) Mem. Variable to 3+ Cyto) Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ Cyto) Specificity: High 4x 20x <u>SF00029783</u></p>	<p>Immunogenicity: Tumor(85%, Variable to 3+ Cyto) Mem. Variable to 3+ Cyto) Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ Cyto) Specificity: High 4x <u>SF000</u></p>

FIG. 26-C

17 (0.2ug/ml)	CAB/GCR6798 (0.2ug/ml)	CAB/GCR8886 (0.196ug/ml)
00%, Variable to 3+ Cyto) lis(Variable to 3+ Cyto) able to 2+ EC) ity: High <u>20x</u> <u>29757</u>	Immunogenicity: Tumor(100%, Variable to 3+ Cyto) Mixed inflammatory cells(Variable to 1+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029753</u>	Immunogenicity: Tumor(100%, Variable Mixed inflammatory cells(Variable to Specificity: High <u>4x</u> <u>20x</u> <u>SF00029754</u>
0%, Variable to 3+ Cyto) ges(Variable to 2+ Cyto) lis(Variable to 2+ Cyto) ity: High <u>20x</u> <u>2975G</u>	Immunogenicity: Tumor(10%, Variable to 2+ Cyto) Intra-alveolar macrophages(Variable to 2+ Cyto) Mixed inflammatory cells(Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029759</u>	Immunogenicity: Tumor(10%, Variable t Intra-alveolar macrophages(Variable to Mixed inflammatory cells(Variable to Specificity: High <u>4x</u> <u>20x</u> <u>SF0002975A</u>
nor(100%, 2+ Cyto) ma(1+ Cyto) ells(Variable to 1+ Cyto) ity: High <u>20x</u> <u>29780</u>	Immunogenicity: Tumor(100%, 2+ Cyto) Cellular stroma(1+ Cyto) Chronic inflammatory cells(Variable to 1+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002977D</u>	Immunogenicity: Tumor(100%, 2+ Cellular stroma(1+ Cyto) Chronic inflammatory cells(Variable to Specificity: High <u>4x</u> <u>20x</u> <u>SF0002977E</u>
15%, Variable to 3+ Cyto) variable to 2+ Cyto) able to 2+ EC) ges(Variable to 2+ Cyto) ity: High <u>20x</u> <u>2978C</u>	Immunogenicity: Tumor(75%, Variable to 3+ Cyto) Cellular Stroma(Variable to 2+ Cyto) Necrosis(Variable to 2+ EC) Intra-alveolar macrophages(Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029789</u>	Immunogenicity: Tumor(75%, Variable t Cellular Stroma(Variable to 2+ C Necrosis(Variable to 2+ EC) Intra-alveolar macrophages(Variable to Specificity: High <u>4x</u> <u>20x</u> <u>SF0002978A</u>
nor(100%, 3+ Cyto) ma(1+ Cyto) able to 3+ EC) ity: High <u>20x</u> <u>29760</u>	Immunogenicity: Tumor(100%, 3+ Cyto) Fibrotic stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002975D</u>	Immunogenicity: Tumor(100%, 3+ Fibrotic stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002975E</u>
x(98%, Variable to 3+ e to 3+ Cyto) anable to 1+ Cyto) nchyma(2+ Cyto) able to 3+ EC) ity: High <u>20x</u> <u>29769</u>	Immunogenicity: Tumor(95%, Variable to 3+ Mem, Variable to 3+ Cyto) Fibrotic stroma(Variable to 1+ Cyto) Normal liver parenchyma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029765</u> Normal liver parenchyma shows positive staining (1+)	Immunogenicity: Tumor(95%, Variab Mem, Variable to 3+ Cyto) Fibrotic stroma(Variable to 1+ C Normal liver parenchyma(1+ Cy Necrosis(Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029766</u> Normal liver parenchyma shows positive s
or(85%, Variable to 3+ e to 3+ Cyto) ma(1+ Cyto) ariable to 2+ Cyto) ity: High <u>20x</u> <u>29784</u>	Immunogenicity: Tumor(95%, Variable to 3+ Mem, Variable to 3+ Cyto) Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029781</u>	Immunogenicity: Tumor(95%, Variab Mem, Variable to 3+ Cyto) Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ C Specificity: High <u>4x</u> <u>20x</u> <u>SF00029782</u>

FIG. 26-D

ml)	No Antibody control (Prediluted)
to 3+ Cyto) 1+ Cyto)	Immunogenicity: N/A Specificity: Unknown <u>SF00029755</u>
to 2+ Cyto) 2+ Cyto) 2+ Cyto)	
Cyto) 1+ Cyto)	
to 3+ Cyto) Cyto) 2+ Cyto)	
Cyto)	
le to 3+ yto) (to)	Immunogenicity: N/A Specificity: Unknown <u>SF00029767</u>
taining (1+) le to 3+ yto)	

FIG. 26-E

<u>CI00000017970</u>	HF1	FR65EE7B3D	Adenocarcinoma of colon
<u>CI00000010013</u>	AF2	FR00028F2E	Adenocarcinoma of pancreas, metastatic
<u>CI00000009651</u>	AF1	FR0002B111	Adenocarcinoma of pancreas, ductal
<u>CI00000008690</u>	CF4	FR00027B0E	Adenocarcinoma of pancreas, ductal
<u>CI00000007678</u>	AF3	FR0002575B	Adenocarcinoma of pancreas, ductal
<u>CI00000009736</u>	AF2	FR0002BAB4	Adenocarcinoma of pancreas, ductal

FIG. 26-F

Adenocarcinoma of colon Grade: AJCC G2: Moderately differentiated Stage: IIIC	Colon/Colon	<u>4X</u> <u>20X</u>	
Adenocarcinoma of pancreas, metastatic Grade: Not Reported Stage: IV	Pancreas/Omentum	<u>4X</u> <u>20X</u>	Immu Fibroes <u>4x</u>
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: IIB	Pancreas/Pancreas	<u>4X</u> <u>20X</u>	
Adenocarcinoma of pancreas, ductal Grade: AJCC G1: Well differentiated Stage: IIA	Pancreas/Pancreas	<u>4X</u> <u>20X</u>	
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: III	Pancreas/Pancreas	<u>4X</u> <u>20X</u>	
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: IIB	Pancreas/Pancreas	<u>4X</u> <u>20X</u>	

FIG. 26-G

	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Cellular stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029787</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Cellular stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029787</u></p>
<p>Immunogenicity: Tumor(100%, 3+ Cyto) Fibroadipose tissue(Variable to 1+ Cyto) Specificity: High</p> <p><u>20x</u> <u>SF0002977C</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Fibroadipose tissue(Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF0002977A</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Fibroadipose tissue(Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF0002977A</u></p>
	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Desmoplastic stroma(Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029771</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Desmoplastic stroma(Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029771</u></p>
	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Myxoid stroma(Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF0002976D</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Myxoid stroma(Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF0002976D</u></p>
	<p>Immunogenicity: Tumor(85%, Variable to 3+ Cyto) Cellular stroma(Variable to 1+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029763</u></p>	<p>Immunogenicity: Tumor(85%, Variable to 3+ Cyto) Cellular stroma(Variable to 1+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029763</u></p>
	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Chronic pancreatitis(Variable to 2+ Cyto) Fibrotic stroma(Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029775</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Chronic pancreatitis(Variable to 2+ Cyto) Fibrotic stroma(Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029775</u></p>

FIG. 26-H

<p>Immunogenicity: Tumor(100%, 3+ Cyto) Cellular stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x <u>29788</u> <u>SF00029785</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Cellular stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x <u>29788</u> <u>SF00029785</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Cellular stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x <u>29788</u> <u>SF00029785</u></p>
<p>Immunogenicity: Tumor(100%, 3+ Cyto) Fibroadipose tissue(Variable to 2+ Cyto) Specificity: High 4x 20x <u>2977B</u> <u>SF00029777</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Fibroadipose tissue(Variable to 2+ Cyto) Specificity: High 4x 20x <u>2977B</u> <u>SF00029777</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Fibroadipose tissue(Variable to 2+ Cyto) Specificity: High 4x 20x <u>2977B</u> <u>SF00029778</u></p>
<p>Immunogenicity: Tumor(100%, 3+ Cyto) Desmoplastic stroma(Variable to 2+ Cyto) Specificity: High 4x 20x <u>29772</u> <u>SF00029770</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Desmoplastic stroma(Variable to 2+ Cyto) Specificity: High 4x 20x <u>29772</u> <u>SF00029770</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Desmoplastic stroma(Variable to 2+ Cyto) Specificity: High 4x 20x <u>29772</u> <u>SF0002976F</u></p>
<p>Immunogenicity: Tumor(100%, 3+ Cyto) Myxoid stroma(Variable to 2+ Cyto) Specificity: High 4x 20x <u>2976E</u> <u>SF0002976B</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Myxoid stroma(Variable to 2+ Cyto) Specificity: High 4x 20x <u>2976E</u> <u>SF0002976B</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Myxoid stroma(Variable to 2+ Cyto) Specificity: High 4x 20x <u>2976E</u> <u>SF0002976C</u></p>
<p>Immunogenicity: Tumor(85%, Variable to 3+ Cyto) Cellular stroma(Variable to 1+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Specificity: High 4x 20x <u>29764</u> <u>SF00029761</u></p>	<p>Immunogenicity: Tumor(85%, Variable to 3+ Cyto) Cellular stroma(Variable to 1+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Specificity: High 4x 20x <u>29764</u> <u>SF00029761</u></p>	<p>Immunogenicity: Tumor(85%, Variable to 3+ Cyto) Cellular stroma(Variable to 1+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Specificity: High 4x 20x <u>29764</u> <u>SF00029762</u></p>
<p>Immunogenicity: Tumor(100%, 3+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Fibrotic stroma(Variable to 1+ Cyto) Specificity: High 4x 20x <u>29776</u> <u>SF00029773</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Fibrotic stroma(Variable to 1+ Cyto) Specificity: High 4x 20x <u>29776</u> <u>SF00029773</u></p>	<p>Immunogenicity: Tumor(100%, 3+ Cyto) Chronic pancreatitis(Variable to 2+ Cyto) Fibrotic stroma(Variable to 2+ Cyto) Specificity: High 4x 20x <u>29776</u> <u>SF00029774</u></p>

FIG. 26-I

Cyto)	
Cyto) Cyto)	Immunogenicity: N/A Specificity: N/A <u>SF00029779</u>
Cyto) + Cyto)	
Cyto) yto)	
to 3+ Cyto) yto) Cyto)	
Cyto) Cyto) yto)	

FIG. 26-7

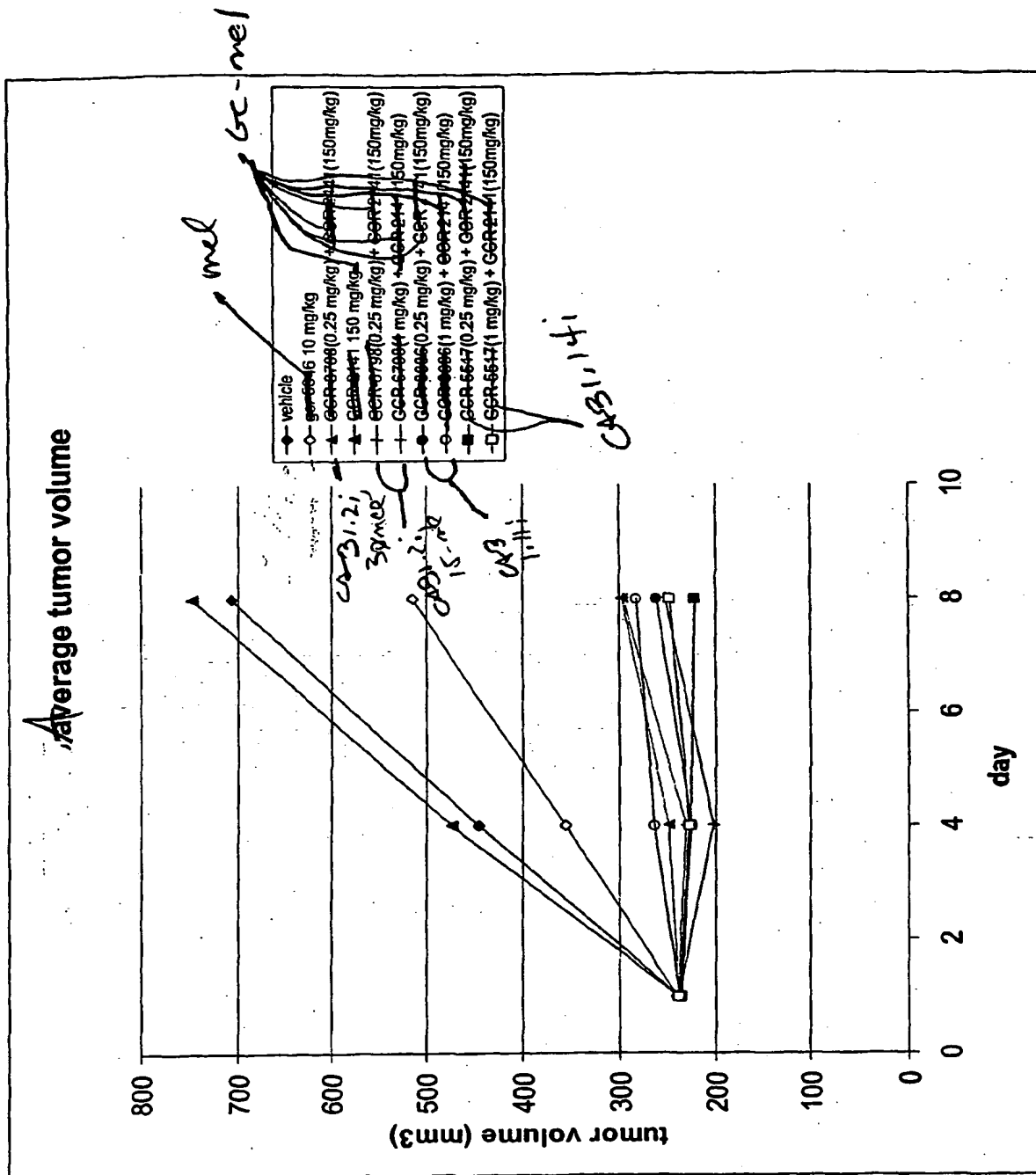


FIGURE 27A

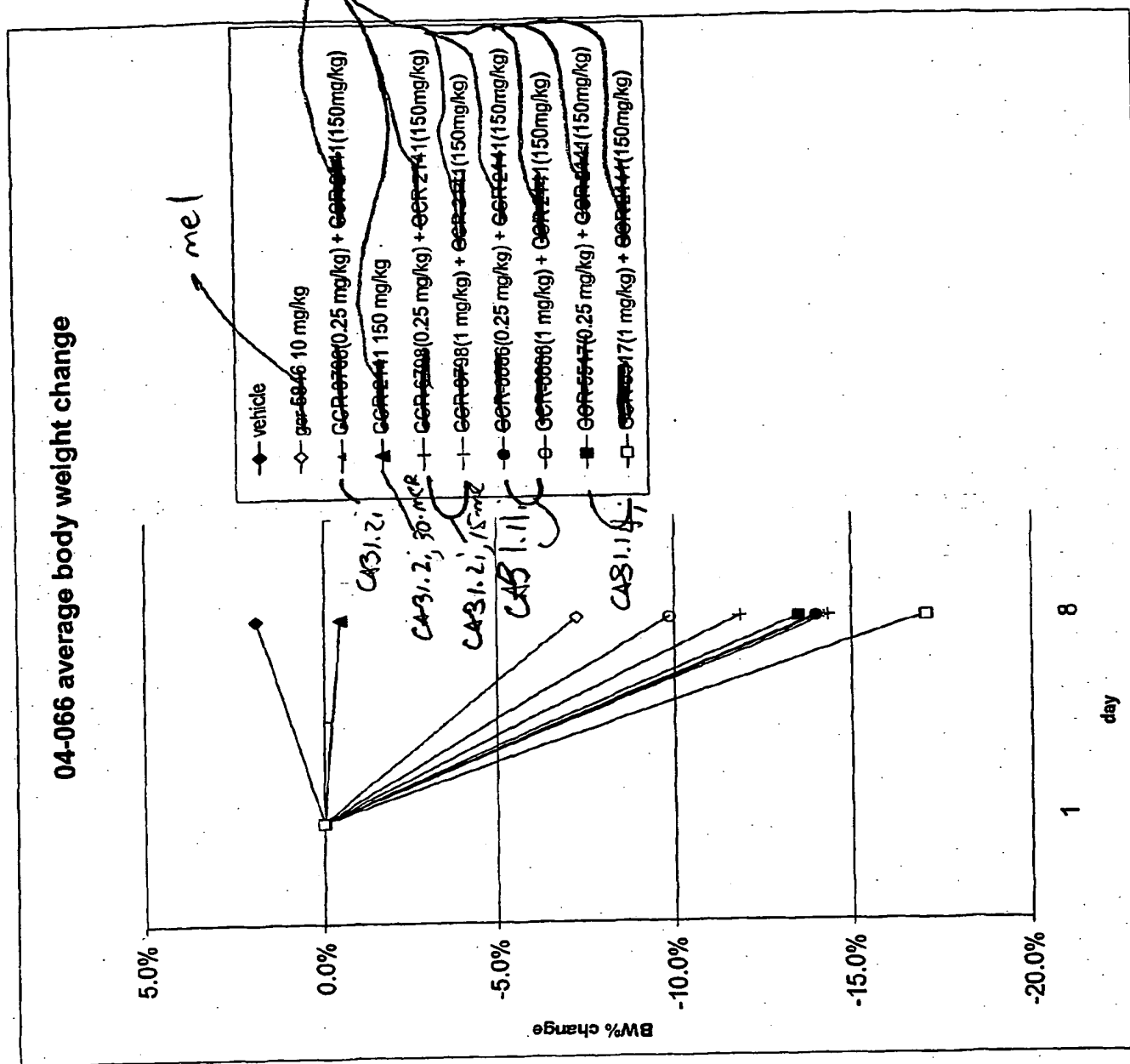


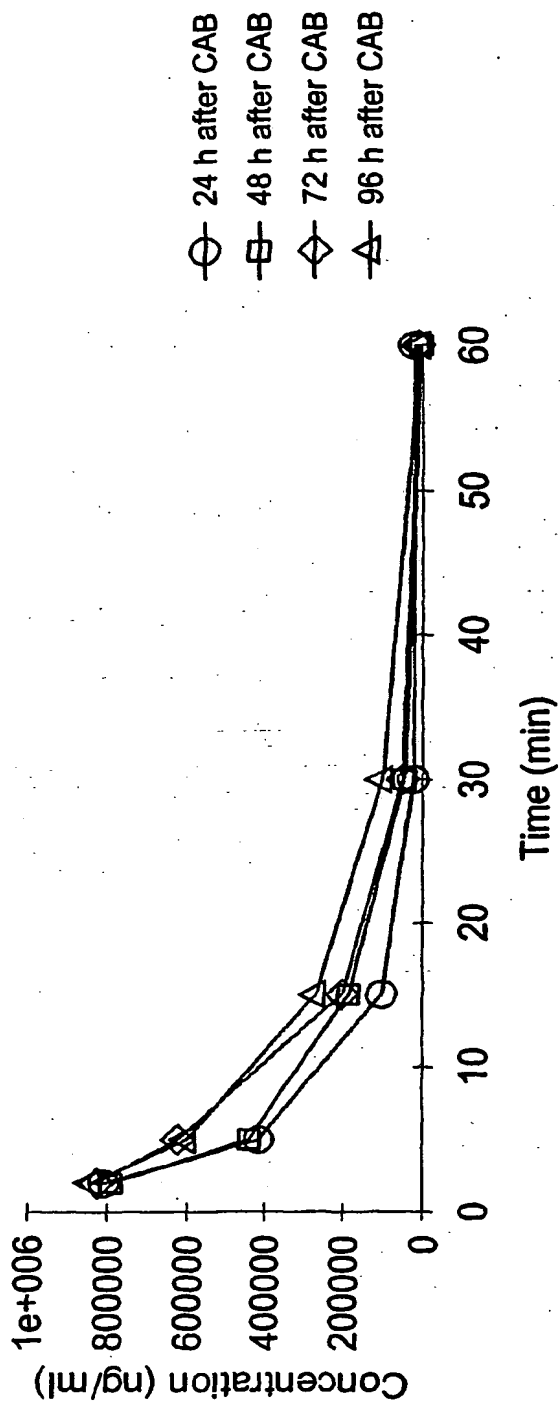
FIGURE 27B

Figure 28

GCR-Me1

Plasma GCR-Me1 concentration-time profiles (linear-linear scale)

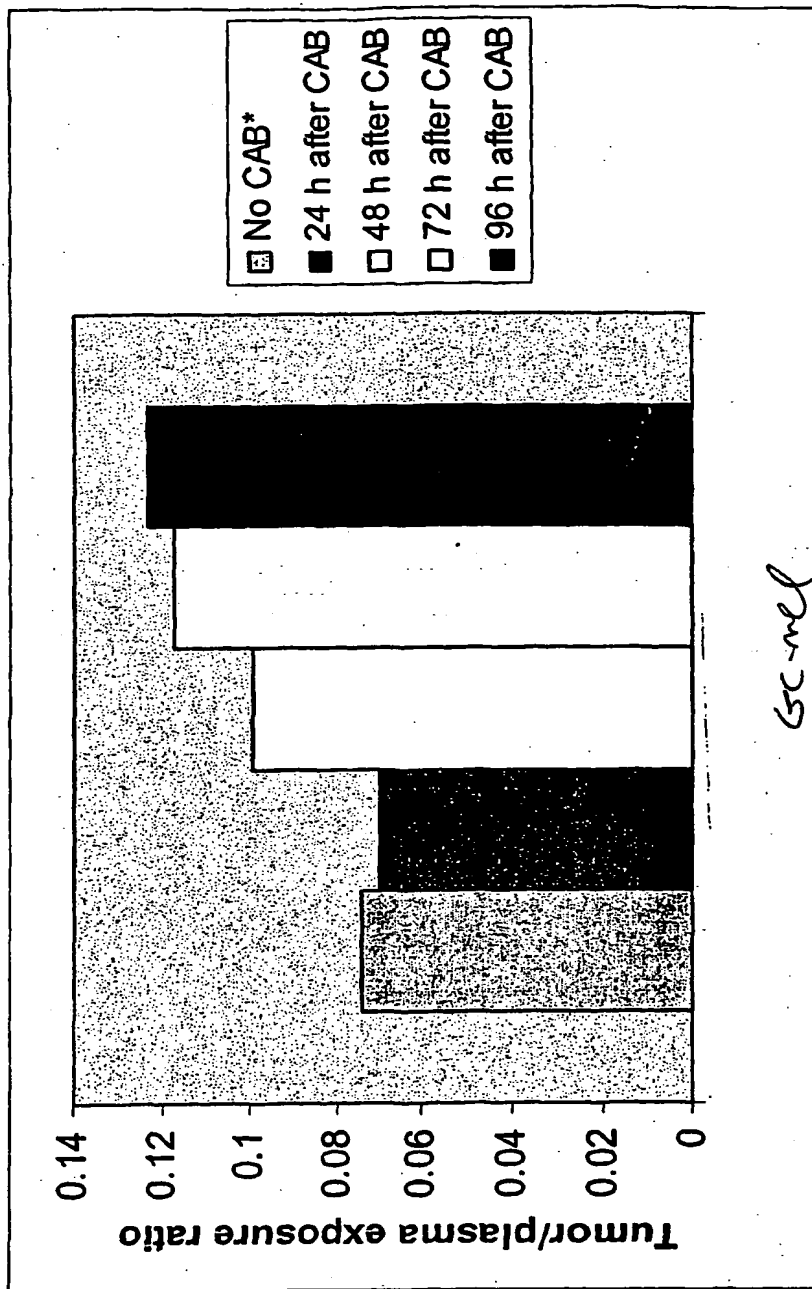
Analyte=GCR2141



US 04/1429

FIG 29A

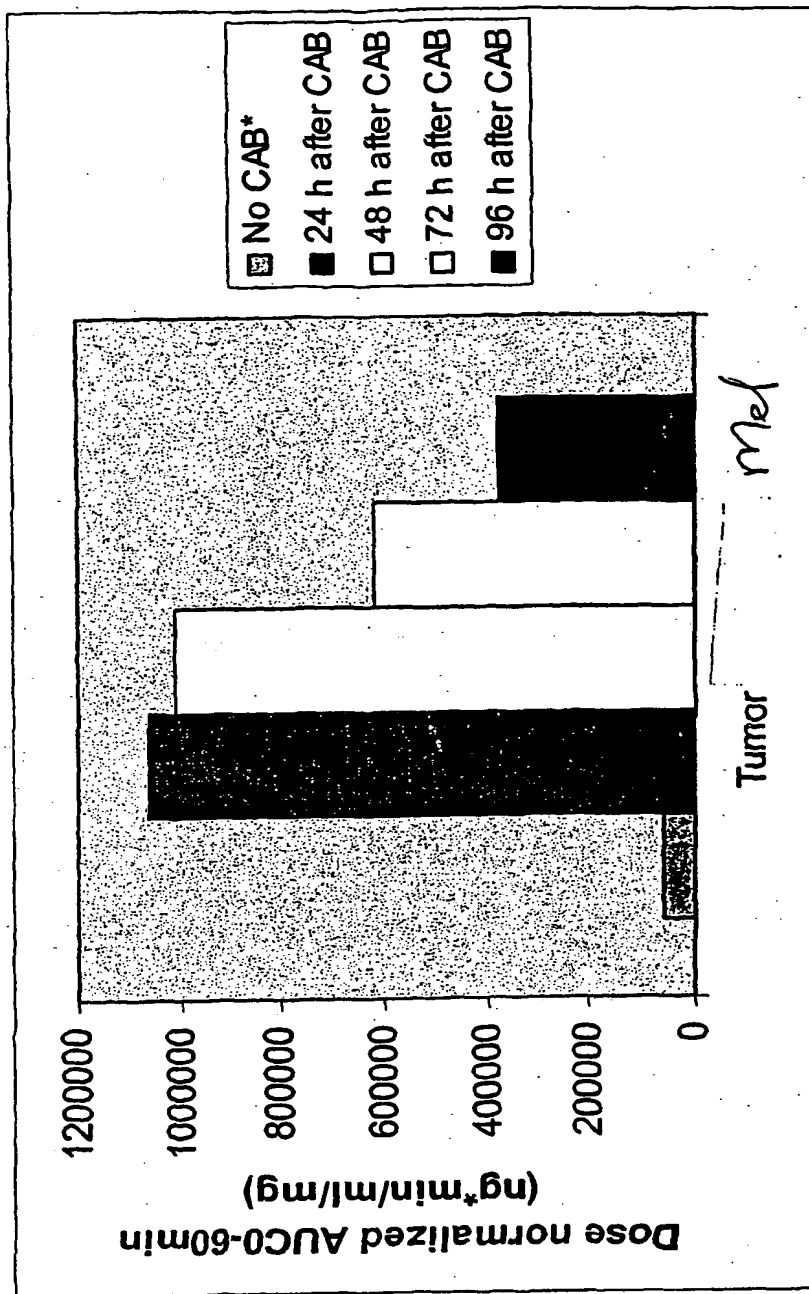
Tumor/Plasma
GC-mel
exposure
ratio



Data from study 04052, melphalan formulated in cyclodextrin

29B

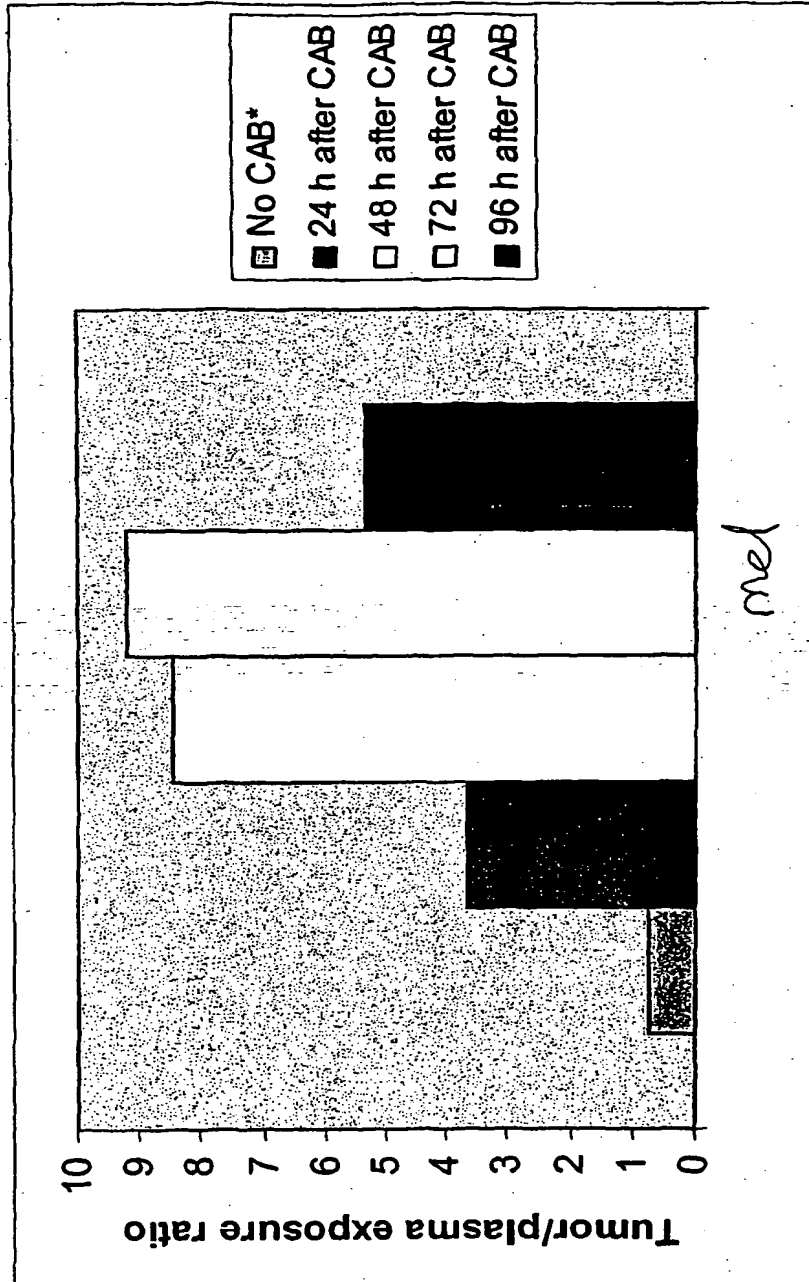
mel
Tumor GCR-5846 exposure after ~~GCR-5846~~ *GCR-mel* administration



* Data from study 04052, melphalan formulated in cyclodextrin

Fig 29C - Tumor/plasma
mel exposure
ratio

GC-mel
Admin



* Data from study 04052, melphalan formulated in cyclodextrin

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